

SEQUENCE LISTING

<110> Rhodes, Kenneth
An, Wenqian

<120> METHODS FOR TREATING CARDIOVASCULAR DISORDERS

<130> MNI-069CP

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<150> USSN 60/110,277

<151> 1998-11-30

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<150> USSN 09/350,614

<151> 1999-07-09

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<170> PatentIn Ver. 2.0

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<212> DNA

<213> Homo sapiens

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<222> (225)..(872)

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ggggggggcc cgggggtccc aatgcgactc aagttcttgc tgcg atg ggg gcc gtc 236
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atg ggg acc ttc tct tct cgg caa acc aaa cca ggg caa ccc tgg aaa 294
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[illegible]

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 35 40 45

Thr Lys Arg Glu Leu Gln Val Leu Tyr Arg Gly Phe Lys Asn Glu Cys
 50 55 60

Pro Ser Gly Val Val Asn Glu Asp Thr Phe Lys Gln Ile Tyr Ala Gln
 65 70 75 80

Phe Phe Pro His Gly Asp Ala Ser Thr Tyr Ala His Tyr Leu Phe Asn
 85 90 95

Ala Phe Asp Thr Thr Gln Thr Gly Ser Val Lys Phe Glu Asp Phe Val
 100 105 110

Thr Ala Leu Ser Ile Leu Leu Arg Gly Thr Val His Glu Lys Leu Arg
 115 120 125

Irp Thr Phe Asn Leu Tyr Asp Ile Asn Lys Asp Gly Tyr Ile Asn Lys
 130 135 140

Glu Glu Met Met Asp Ile Val Lys Ala Ile Tyr Asp Met Met Gly Lys
 145 150 155 160

Tyr Thr Tyr Pro Val Leu Lys Glu Asp Thr Pro Arg Gln His Val Asp
 165 170 175

Val Phe Phe Gln Lys Met Asp Lys Asn Lys Asp Gly Ile Val Thr Leu
 180 185 190

Asp Glu Phe Leu Glu Ser Cys Gln Glu Asp Asp Asn Ile Met Arg Ser
 195 200 205

Leu Gln Leu Phe Gln Asn Val Met
 210 215

See the last two Ar; Gly Thr Val His Ala Lys Leu Arg Trp Thr Phe
146 153 159 160

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 Met Asp Ile Val Lys Ala Ile Tyr Asp Met Met Gly Lys Tyr Thr Tyr
 180 185 190
 atg gat atc aaa gag gat atc atc atc atc atc atc atc atc atc atc atc 923
 Ile Val Leu Lys Glu Asp Thr Pro Arg Glu His Val Asp Val His His
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 gag aaa atg gat aaa atc aaa gat ggc att gta atc tta tta tta tta 971
 Gln Lys Met Asp Lys Asn Lys Asp Gly Ile Val Thr Leu Asp Glu Phe
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 atc gag tat tgc gag gat gat atc atc atc atc atc atc atc atc atc atc 1019
 Leu Glu Ser Cys Gln Glu Asp Asp Asn Ile Met Arg Ser Leu Glu Leu
 225 230 235 240
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 Phe Gln Asn Val Met
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 aa 1860

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- 1911: 5
- 1912: 1407
- 1913: 191A
- 1914: 191S, 191S, 191S

1. 1990年12月25日，在“中国改革二十年”论坛上，江泽民总书记在会上的讲话中，第一次提出“社会主义市场经济”的概念。

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ttc gac acc acc cag aca ggc tct gta aag ttc gag gac ttt gtg act 815	
Phe Asp Thr Thr Gln Thr Gly Ser Val Lys Phe Glu Asp Phe Val Thr	
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gct ctg tgg att tta ctg aga ggg aca gtc cat gaa aaa cta agg tgg 863	
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Thr Tyr Pro Val Leu Lys Glu Asp Thr Pro Arg Gln His Val Asp Val	
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Phe Phe Gln Lys Met Asp Lys Asn Lys Asp Gly Ile Val Thr Leu Asp	
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 Gln Leu Phe Gln Asn Val Met
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 35 40 45
 Thr Lys Arg Glu Leu Gln Val Leu Tyr Arg Gly Phe Lys Asn Glu Cys
 50 55 60
 Pro Ser Gly Val Val Asn Glu Glu Thr Phe Lys Gln Ile Tyr Ala Gln
 65 70 75 80
 Phe Phe Pro His Gly Asp Ala Ser Thr Tyr Ala His Tyr Leu Phe Asn
 85 90 95

Ala Phe Asp Thr Thr Gln Thr Gly Ser Val Lys Phe Glu Asp Phe Val
 100 130 110
 Thr Ala Leu Ser Ile Leu Leu Arg Gly Thr Val His Glu Lys Thr Arg
 115 120 125
 Trp Thr Phe Asn Leu Tyr Asp Ile Asn Lys Asp Gly Tyr Ile Asn Lys
 130 135 140
 Glu Glu Met Met Asp Ile Val Lys Ala Ile Tyr Asp Met Met Gly Lys
 145 150 155 160
 Tyr Thr Tyr Pro Val Leu Lys Glu Asp Thr Pro Arg Gln His Val Asp
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 Val Phe Phe Gln Lys Met Asp Lys Asn Lys Asp Gly Ile Val Thr Leu
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 tgg tat tac cag tat cag aga gac aag atc gag gat gat ctg gag atg 150
 Trp Tyr Tyr Gln Tyr Gln Arg Asp Lys Ile Glu Asp Asp Leu Glu Met
 25 30 35 40
 acc atg gtt tgc cat cgg cct gag aga ctg gag cag ctt gag gca cag 198
 Thr Met Val Cys His Arg Pro Glu Gly Leu Glu Gln Leu Glu Ala Gln
 45 50 55
 atg aac ttc atc aag aga gaa ctg caa gtc ctt tac cgg gga ttc aaa 246
 Thr Asn Phe Thr Lys Arg Glu Leu Gln Val Leu Tyr Arg Gly Phe Lys
 60 65 70
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 75 80 85

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 90 95 100
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 aaa ctg agg tgg aag ttt aat ttg tac gac atc aat aaa gac ggc tac 486
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 185 190 195 200
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Gly Leu Glu Gln Leu Glu Ala Gln Thr Asn Phe Thr Lys Arg Gln Leu
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Gln Val Leu Tyr Arg Gly Phe Lys Asn Glu Cys Pro Ser Gly Val Val
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Asn Glu Glu Thr Phe Lys Gln Ile Tyr Ala Gln Phe Phe Pro His Gly
85 90 95

Asp Ala Ser Thr Tyr Ala His Tyr Leu Phe Asn Ala Phe Asp Thr Thr
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Gln Thr Gly Ser Val Lys Phe Glu Asp Phe Val Thr Ala Leu Ser Ile
115 120 125

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Tyr Asp Ile Asn Lys Asp Gly Tyr Ile Asn Lys Glu Glu Met Met Asp
145 150 155 160

Ile Val Lys Ala Ile Tyr Asp Met Met Gly Lys Tyr Thr Tyr Pro Val
165 170 175

Leu Lys Glu Asp Thr Pro Arg Gln His Val Asp Val Phe Phe Gln Lys
180 185 190

Met Asp Lys Asn Lys Asp Gly Ile Val Thr Leu Asp Gln Ile Leu Gln
195 200 205

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tat cag aga gac aag att gag gat gag cta gag atg acc atg gtt tgc 208

Tyr Gln Arg Asp Lys Ile Glu Asp Glu Leu Glu Met Thr Met Val Cys

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cac cgg cct gag gga ctg gag cag ctt gag gca cag acg aac ttc acc 256

His Arg Pro Glu Gly Leu Glu Gln Leu Glu Ala Gln Thr Asn Phe Thr

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aag aga gaa ctg caa gtc ttg tac cgg gga ttc aaa aac gag tgc cct 304

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Ser Gly Val Val Asn Glu Glu Thr Phe Lys Gln Ile Tyr Ala Gln Phe

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100

105

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Ala Leu Ser Ile Leu Leu Arg Gly Thr Val His Glu Lys Leu Arg Trp

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Gln Val Leu Tyr Arg Gly Phe Lys Asn Glu Cys Pro Ser Gly Val Val
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Asn Glu Glu Thr Phe Lys Gln Ile Tyr Ala Gln Phe Phe Pro His Gly
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Asp Ala Ser Thr Tyr Ala His Tyr Leu Ile Asn Ala Ile Asp Thr Thr
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Ile Thr Ile Ala Val Tyr Leu Glu Arg Leu Thr Thr Ile Thr Thr Thr
120 121 122

Leu Leu Arg Gly Thr Val His Glu Lys Leu Arg Trp Thr Phe Asn Leu
130 135 140

Tyr Asp Ile Asn Lys Asp Gly Tyr Ile Asn Lys Glu Glu Met Met Asp
145 150 155 160

Ile Val Lys Ala Ile Tyr Asp Met Met Gly Lys Tyr Thr Tyr Ile Val
165 170 175

Leu Lys Glu Asp Thr Pro Arg Gln His Val Asp Val Phe Phe Gln Lys
180 185 190

Met Asp Lys Asn Lys Asp Gly Ile Val Thr Leu Asp Glu Phe Leu Glu
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Asn Val Met
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<222> (345)..(953)

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sequence may be any amino acid

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gttagagga ttgtgtgga ggttgagta caaataggg agttatagc ttatgttgg 240

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440
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445
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 64 65 66 67 68 69

470
 Thr Glu Thr Gly Ser Val Lys Phe Glu Asp Phe Val Thr Ala Leu Ser
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480
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 81 82 83 84 85 86

485
 Asp Ile Val Lys Ala Ile Tyr Asp Met Met Gly Lys Tyr Thr Tyr Leu
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Asp Leu Ser Asp Arg Lys Ile Glu Asp Arg Leu Glu Met Thr Met Val
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 Cys His Arg Ile Glu Gly Leu Glu Gln Leu Glu Ala Gln Thr Asn Pro
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 Thr Lys Arg Glu Leu Gln Val Leu Tyr Arg Gly Ile Lys Asn Glu Cys
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 Pro Ser Gly Val Val Asn Glu Glu Thr Ile Lys Val Ile Tyr Ala Gln
 85 90 95
 Phe Ile Pro His Gly Asp Ala Ser Thr Tyr Ala His Tyr Leu Ile Asn
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 Ala Phe Asp Thr Thr Gln Thr Gly Ser Val Lys Ile Glu Asp Phe Val
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 Thr Ala Leu Ser Ile Leu Leu Arg Gly Thr Val His Glu Lys Leu Lys
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 Trp Thr Phe Asn Leu Tyr Asp Ile Asn Lys Asp Gly Tyr Ile Asn Lys
 145 150 155 160
 Glu Glu Met Met Asp Ile Val Lys Ala Ile Tyr Asp Met Met Gly Lys
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 Leu Ala Ala Pro Ala Ser Leu Arg Pro His Arg Pro Arg Leu Leu Asp
 9' 7c

Cys Gln Asp Arg Gly Gln Gln Gln Ile Gln Lys Trp Asp Gly Tyr Ser Arg 473
 Pro Asp Ser Val Asp Asp Glu Phe Glu Leu Ser Thr Val Cys His Arg
 75 80 85

Cct gag ggt ctg gag cag ctg cag gag cca acc aaa ttc acg cgt aag 521
 Pro Glu Gly Leu Glu Gln Leu Gln Glu Gln Thr Lys Phe Thr Arg Lys
 90 95 100 105

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Glu Leu Gln Val Leu Tyr Arg Gly Phe Lys Asn Glu Cys Pro Ser Gly
110 115 120

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ile Val Asn Glu Glu Asn Phe Lys Gln Ile Tyr Ser Gln Phe Phe Pro
125 130 135

Caa gga gac tcc agc acc tat gcc act ttt ctc ttc aat gcc ttt gac 665
 Gln Gly Asp Ser Ser Thr Tyr Ala Thr Phe Leu Phe Asn Ala Phe Asp
 140 145 150

acc aac cat gat ggc tgg gtc art ttt gag gac ttt gtg gct ggt ttg 713
Thr Asn His Asp Gly Ser Val Ser Phe Glu Asp Phe Val Ala Gly Leu
155 160 165

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 Ser Val Ile Leu Arg Gly Thr Val Asp Asp Arg Leu Asn Trp Ala Phe
 170 175 180 185

aac ctg tat gac ctt aac ang gac ggc ttc atc acc aag gag gaa atg 809
 Asn Leu Tyr Asp Leu Asn Lys Asp Gly Cys Ile Thr Lys Glu Glu Met
 140 146 200

Met Asp Ala Arg Asn Asp Glu His Ile Lys Leu Phe Pro Ser Thr Val
 Met Asp His Met Lys Ser Thr Tyr Asn Met Met Gly Lys Tyr Thr Tyr

Net you die egg bag bag the air all die had gty bag egg the the 905
Pro Ala Den Ann Ala Ala Ala Pro Ann Ala His Val Ala Ser The The
211 226 231

141 543 513 503 493 483 473 463 453 443 433 423 413 403 393 383 373 363 353 343 333 323 313 303 293 283 273 263 253 243 233 223 213 203 193 183 173 163 153 143 133 123 113 103 93 83 73 63 53 43 33 23 13 3
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Gln Ala Leu Ile Ser Val Ser Gln Thr Leu Ala Ala Pro Ala Ser Leu
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Arg Pro His Arg Pro Arg Leu Leu Asp Pro Asp Ser Val Asp Asp His
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Ala Gln Gln Thr Lys His Thr Arg Lys Glu Leu His Val Leu Tyr Arg
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Gly Phe Lys Asn Gln Cys Pro Ser Gly Ile Val Asn Gln Gln Asn Phe
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Lys Gln Ile Tyr Ser Gln Phe Phe Pro Gln Gly Asp Ser Ser Thr Tyr
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Ala Thr Phe Leu Phe Asn Ala Phe Asp Thr Asn His Asp Gly Ser Val
145 150 155 160

Ser Phe Gln Asp Phe Val Ala Gly Leu Ser Val Ile Leu Arg Gly Thr
165 170 175

Val Asp Asp Arg Leu Asn Tyr Ala Phe Asn Leu Tyr Asp Leu Asn Lys
180 185 190

Asp Gly Cys Ile Thr Lys Gln Glu Met Leu Asp Ile Met Lys Ser Ile
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Tyr Asp Met Met Gly Lys Tyr Thr Tyr Pro Ala Leu Arg Glu Glu Ala
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Pro Arg Glu His Val Glu Ser Phe Phe Gln Lys Met Asp Arg Asn Lys
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Pro Ser Lys Lys Ala Leu Lys Gln Arg Phe Leu Lys Leu Pro Cys
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tac agt ccc cca gtt cta cca tca gta agt gaa aca tta tta tta cca 145
Cys Gly Pro Gln Ala Leu Pro Ser Val Ser Gln Thr Leu Ala Ala Pro
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tct tca cta cta cta cta cta cta cta cta cta cta cta cta cta 192
Ala Ser Leu Arg Pro His Arg Pro Arg Pro Leu Asp Pro Asp Ala Val
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titration of the protein solution with 0.1M NaOH solution at pH 7.0.
 The protein solution was then dialyzed into 0.1M NaOH solution at pH 7.0.
 1.47

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 Ala Ser Leu Arg Pro His Arg Pro Arg Pro Leu Asp Pro Asp Ser Val
 50 55 60
 Glu Asp Glu Phe Glu Leu Ser Thr Val Cys His Arg Pro Gln Gly Leu
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 Glu Gln Leu Gln Glu Gln Thr Lys Phe Thr Arg Arg Glu Leu Gln Val
 85 90 95
 Leu Tyr Arg Gly Phe Lys Asn Glu Cys Pro Ser Gly Ile Val Asn Glu
 100 105 110
 Glu Asn Phe Lys Gln Ile Tyr Ser Gln Phe Phe Pro Gln Gly Asp Ser
 115 120 125
 Ser Asn Tyr Ala Thr Phe Leu Phe Asn Ala Phe Asp Thr Asn His Asp
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 Gly Ser Val Ser Phe Glu Asp Phe Val Ala Gly Leu Ser Val Ile Leu
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 Leu Asn Lys Arg Gly Cys Ile Thr Lys Glu Gln Met Leu Asp Ile Met
 180 185 190
 Lys Ser Ile Tyr Asp Met Met Gly Lys Tyr Thr Tyr Pro Ala Leu Arg
 195 200 205
 Gln Gln Ala Pro Arg Gln His Val Gln Ser Phe Phe Gln Lys Met Arg
 210 215 220
 Arg Asn Lys Arg Gly Val Val Thr Ile Gln Gln Phe Ile Gln Ser Cys
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<220>

<221> CDS

<222> (181)..(990)

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gac ggc tcc tat gac cag ctt acg ggc cac cct cca ggg ccc agt aaa    276
Asp Gly Ser Tyr Asp Gln Leu Thr Gly His Pro Pro Gly Pro Ser Lys
   20             25             30

aaa gcc ctg aag cag cgt ttc ctc aag ctg ctg ccg tgc tgc ggg ccc    324
Lys Ala Leu Lys Gln Arg Phe Leu Lys Leu Leu Pro Cys Cys Gly Pro
   35             40             45

caa gcc ctg ccc tca gtc agt gaa aca tta gct gcc cca gcc tcc ctc    372
Gln Ala Leu Pro Ser Val Ser Glu Thr Leu Ala Ala Pro Ala Ser Leu
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cgc ccc cac aga ccc cgc ccg ctg gac cca gac agc gtg gag gat gag    420
Arg Pro His Arg Pro Arg Pro Leu Asp Pro Asp Ser Val Glu Asp Glu
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ttt gaa cta tcc acg gtg tcc cac cgg cct gag ggt ctg gaa caa ctc    468
Phe Glu Leu Ser Thr Val Cys His Arg Pro Glu Gly Leu Glu Gln Leu
   85             90             95

cag gaa caa acc aag ttc aca cgc aga gag ttg cag gtc ctg tac aga    516
Gln Glu Gln Thr Lys Phe Thr Arg Arg Glu Leu Gln Val Leu Tyr Arg
  100             105             110

ggc ttc aag aac gaa tgt ccc agc gga att gtc aac gag gaa aac ttc    564
Gly Phe Lys Asn Glu Cys Pro Ser Gly Ile Val Asn Glu Glu Asn Phe
  115             120             125

aag caa att tat tct cag ttc ttt ccc caa gga gac tct agt aac tac    612
Lys Gln Ile Tyr Ser Gln Phe Phe Pro Gln Gly Asp Ser Ser Asn Tyr
  130             135             140

att att ttt ctc ttc aat gaa ttt gaa aac aat tat gat gtt ttt atc    660
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  145             150             155             160

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Asp Gly Val Val Thr Ile Glu Glu Phe Ile Glu Ser Cys Gln Gln Asp
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Phe Ala His Arg Arg Trp Arg Ser Cys Ile Phe Val Asn Lys
 Glu Asn Ile Met Arg Ser Met Gln Leu Phe Asp Asn Val Ile
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[illegible]

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1. The following information is provided for the year ended 31/12/2019:

ALL INFORMATION CONTAINED HEREIN IS UNCLASSIFIED DATE 07-14-2011 BY 60322 UCBAW

07-06-1981 - two dates changed at collector's request; all pages 1410

Journal of Management Inquiry 18(6) 709–724

[illegible]

1. The first step is to identify the problem or question that needs to be answered. This involves understanding the context and the specific requirements of the task.

[illegible]

* "The following information was obtained from the records of the Department of Social Services, New York City, dated 10/17/68:

* * * * *

11. *Chlorophyll *a* and *b* content* were determined by the method of Arar and Lee (1993) using a spectrophotometer (Shimadzu 1601) at 663 and 646 nm. The chlorophyll content was expressed as mg g⁻¹ of fresh weight.

1. 2. 3. 4. 5. 6. 7. 8. 9. 10. 11. 12. 13. 14. 15. 16. 17. 18. 19. 20. 21. 22. 23. 24. 25. 26. 27. 28. 29. 30. 31. 32. 33. 34. 35. 36. 37. 38. 39. 40. 41. 42. 43. 44. 45. 46. 47. 48. 49. 50. 51. 52. 53. 54. 55. 56. 57. 58. 59. 60. 61. 62. 63. 64. 65. 66. 67. 68. 69. 70. 71. 72. 73. 74. 75. 76. 77. 78. 79. 80. 81. 82. 83. 84. 85. 86. 87. 88. 89. 90. 91. 92. 93. 94. 95. 96. 97. 98. 99. 100. 101. 102. 103. 104. 105. 106. 107. 108. 109. 110. 111. 112. 113. 114. 115. 116. 117. 118. 119. 120. 121. 122. 123. 124. 125. 126. 127. 128. 129. 130. 131. 132. 133. 134. 135. 136. 137. 138. 139. 140. 141. 142. 143. 144. 145. 146. 147. 148. 149. 150. 151. 152. 153. 154. 155. 156. 157. 158. 159. 160. 161. 162. 163. 164. 165. 166. 167. 168. 169. 170. 171. 172. 173. 174. 175. 176. 177. 178. 179. 180. 181. 182. 183. 184. 185. 186. 187. 188. 189. 190. 191. 192. 193. 194. 195. 196. 197. 198. 199. 200. 201. 202. 203. 204. 205. 206. 207. 208. 209. 210. 211. 212. 213. 214. 215. 216. 217. 218. 219. 220. 221. 222. 223. 224. 225. 226. 227. 228. 229. 230. 231. 232. 233. 234. 235. 236. 237. 238. 239. 240. 241. 242. 243. 244. 245. 246. 247. 248. 249. 250. 251. 252. 253. 254. 255. 256. 257. 258. 259. 260. 261. 262. 263. 264. 265. 266. 267. 268. 269. 270. 271. 272. 273. 274. 275. 276. 277. 278. 279. 280. 281. 282. 283. 284. 285. 286. 287. 288. 289. 290. 291. 292. 293. 294. 295. 296. 297. 298. 299. 300. 301. 302. 303. 304. 305. 306. 307. 308. 309. 310. 311. 312. 313. 314. 315. 316. 317. 318. 319. 320. 321. 322. 323. 324. 325. 326. 327. 328. 329. 330. 331. 332. 333. 334. 335. 336. 337. 338. 339. 340. 341. 342. 343. 344. 345. 346. 347. 348. 349. 350. 351. 352. 353. 354. 355. 356. 357. 358. 359. 360. 361. 362. 363. 364. 365. 366. 367. 368. 369. 370. 371. 372. 373. 374. 375. 376. 377. 378. 379. 380. 381. 382. 383. 384. 385. 386. 387. 388. 389. 390. 391. 392. 393. 394. 395. 396. 397. 398. 399. 400. 401. 402. 403. 404. 405. 406. 407. 408. 409. 410. 411. 412. 413. 414. 415. 416. 417. 418. 419. 420. 421. 422. 423. 424. 425. 426. 427. 428. 429. 430. 431. 432. 433. 434. 435. 436. 437. 438. 439. 440. 441. 442. 443. 444. 445. 446. 447. 448. 449. 450. 451. 452. 453. 454. 455. 456. 457. 458. 459. 460. 461. 462. 463. 464. 465. 466. 467. 468. 469. 470. 471. 472. 473. 474. 475. 476. 477. 478. 479. 480. 481. 482. 483. 484. 485. 486. 487. 488. 489. 490. 491. 492. 493. 494. 495. 496. 497. 498. 499. 500. 501. 502. 503. 504. 505. 506. 507. 508. 509. 510. 511. 512. 513. 514. 515. 516. 517. 518. 519. 520. 521. 522. 523. 524. 525. 526. 527. 528. 529. 530. 531. 532. 533. 534. 535. 536. 537. 538. 539. 540. 541. 542. 543. 544. 545. 546. 547. 548. 549. 550. 551. 552. 553. 554. 555. 556. 557. 558. 559. 560. 561. 562. 563. 564. 565. 566. 567. 568. 569. 570. 571. 572. 573. 574. 575. 576. 577. 578. 579. 580. 581. 582. 583. 584. 585. 586. 587. 588. 589. 590. 591. 592. 593. 594. 595. 596. 597. 598. 599. 600. 601. 602. 603. 604. 605. 606. 607. 608. 609. 610. 611. 612. 613. 614. 615. 616. 617. 618. 619. 620. 621. 622. 623. 624. 625. 626. 627. 628. 629. 630. 631. 632. 633. 634. 635. 636. 637. 638. 639. 640. 641. 642. 643. 644. 645. 646. 647. 648. 649. 650. 651. 652. 653. 654. 655. 656. 657. 658. 659. 660. 661. 662. 663. 664. 665. 666. 667. 668. 669. 670. 671. 672. 673. 674. 675. 676. 677. 678. 679. 680. 681. 682. 683. 684. 685. 686. 687. 688. 689. 690. 691. 692. 693. 694. 695. 696. 697. 698. 699. 700. 701. 702. 703. 704. 705. 706. 707. 708. 709. 710. 711. 712. 713. 714. 715. 716. 717. 718. 719. 720. 721. 722. 723. 724. 725. 726. 727. 728. 729. 730. 731. 732. 733. 734. 735. 736. 737. 738. 739. 740. 741. 742. 743. 744. 745. 746. 747. 748. 749. 750. 751. 752. 753. 754. 755. 756. 757. 758. 759. 760. 761. 762. 763. 764. 765. 766. 767. 768. 769. 770. 771. 772. 773. 774. 775. 776. 777. 778. 779. 780. 781. 782. 783. 784. 785. 786. 787. 788. 789. 790. 791. 792. 793. 794. 795. 796. 797. 798. 799. 800. 801. 802. 803. 804. 805. 806. 807. 808. 809. 810. 811. 812. 813. 814. 815. 816. 817. 818. 819. 820. 821. 822. 823. 824. 825. 826. 827. 828. 829. 830. 831. 832. 833. 834. 835. 836. 837. 838. 839. 840.

* χ^2 test for independence: $\chi^2 = 1.14$, $df = 1$, $p = 0.286$. χ^2 test for independence: $\chi^2 = 0.00$, $df = 1$, $p = 0.999$.

1. The first part of the paper is devoted to the study of the asymptotic behavior of the solutions of the system (1) as $t \rightarrow \infty$. It is shown that the solutions of the system (1) are bounded and tend to zero as $t \rightarrow \infty$ if and only if the matrix A is stable. The second part of the paper is devoted to the study of the asymptotic behavior of the solutions of the system (1) as $t \rightarrow \infty$ if the matrix A is not stable. It is shown that the solutions of the system (1) are bounded and tend to zero as $t \rightarrow \infty$ if and only if the matrix A is stable.

1. The first step is to identify the problem or question that needs to be answered. This involves understanding the context and the specific requirements of the task.

2. Next, it is important to gather relevant information and data. This can be done through research, consultation with experts, or by analyzing existing data sets.

3. Once the information is gathered, the next step is to analyze it. This involves identifying patterns, trends, and relationships that can help in understanding the problem.

4. After analysis, the next step is to develop a solution or plan. This involves identifying the most effective and efficient way to address the problem.

5. Finally, the solution is implemented and the results are evaluated. This involves monitoring the progress and making adjustments as needed to ensure the solution is effective.

6. The last step is to document the process and results. This involves creating a report or record that details the steps taken and the outcomes achieved.

7. The final step is to share the results with the relevant stakeholders. This involves presenting the findings and recommendations to the appropriate audience.

8. The final step is to review the process and results. This involves reflecting on the experience and identifying areas for improvement for future projects.

9. The final step is to conclude the project. This involves summarizing the key findings and recommendations and ensuring all tasks are completed.

10. The final step is to archive the project. This involves storing the project files and documents in a secure and accessible location for future reference.

[illegible]

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Asp Gly Ser Tyr Asp Gln Leu Thr Gly His Pro Pro Gly Pro Ser Lys
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Thr Glu Leu Ser Thr Val Cys His Arg Pro Glu Gly Leu Glu Glu Leu
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Gln Gln Gln Thr Lys Phe Thr Arg Arg Gln Leu Gln Val Leu Tyr Arg
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Gly Phe Lys Asn Gln Cys Pro Ser Gly Ile Val Asn Gln Gln Asn Phe
112 113 114

Tyr His Ile Tyr Ser Glu Thr Thr Trp Glu Gly Asp Ser Met Asn Tyr
 139 185 191

Ala Thr Ile Leu Ile Asn Ala Phe Asp Thr Asn His Asp Gly Ser Val
145 150 155

Gen. Eth. GLN Amt: Etn. Val. Alt. Fly. Det. Ser. Val. Ctr. Det. Amt: Fly. Thr.

The Asp Asp Arg Lys Asp Tyr Ala His Arg Lys Tyr Asp Lys Arg Lys
 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20

Asp Gly Cys Ile Thr Lys Glu His Met Leu Asp Ile Met Lys Arg Ile

Typ. Age: Most Most Fly Age: Typ. The Typ. In. All In. In. All In. In. All

| 117 | 118 | 119 | 120 | 121 | 122 | 123 | 124 | 125 | 126 | 127 | 128 | 129 | 130 | 131 | 132 | 133 | 134 | 135 | 136 | 137 | 138 | 139 | 140 | 141 | 142 | 143 | 144 | 145 | 146 | 147 | 148 | 149 | 150 | 151 | 152 | 153 | 154 | 155 | 156 | 157 | 158 | 159 | 160 | 161 | 162 | 163 | 164 | 165 | 166 | 167 | 168 | 169 | 170 | 171 | 172 | 173 | 174 | 175 | 176 | 177 | 178 | 179 | 180 | 181 | 182 | 183 | 184 | 185 | 186 | 187 | 188 | 189 | 190 | 191 | 192 | 193 | 194 | 195 | 196 | 197 | 198 | 199 | 200 | 201 | 202 | 203 | 204 | 205 | 206 | 207 | 208 | 209 | 210 | 211 | 212 | 213 | 214 | 215 | 216 | 217 | 218 | 219 | 220 | 221 | 222 | 223 | 224 | 225 | 226 | 227 | 228 | 229 | 230 | 231 | 232 | 233 | 234 | 235 | 236 | 237 | 238 | 239 | 240 | 241 | 242 | 243 | 244 | 245 | 246 | 247 | 248 | 249 | 250 | 251 | 252 | 253 | 254 | 255 | 256 | 257 | 258 | 259 | 260 | 261 | 262 | 263 | 264 | 265 | 266 | 267 | 268 | 269 | 270 | 271 | 272 | 273 | 274 | 275 | 276 | 277 | 278 | 279 | 280 | 281 | 282 | 283 | 284 | 285 | 286 | 287 | 288 | 289 | 290 | 291 | 292 | 293 | 294 | 295 | 296 | 297 | 298 | 299 | 300 |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
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| | | | | | | | | | | | | | | | |
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| Asp | Gly | Ser | Tyr | Asp | Gln | Leu | Thr | Gly | His | Pro | Pro | Gly | Pro | Thr | Lys |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Lys | Ala | Leu | Lys | Gln | Arg | Phe | Leu | Lys | Leu | Leu | Pro | Cys | Cys | Gly | Pro |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Gln | Ala | Leu | Pro | Ser | Val | Ser | Glu | Asn | Ser | Val | Asp | Asp | Glu | Phe | Glu |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Leu | Ser | Thr | Val | Cys | His | Arg | Pro | Glu | Gly | Leu | Glu | Gln | Leu | Gln | Glu |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 |
| Gln | Thr | Lys | Phe | Thr | Arg | Lys | Glu | Leu | Gln | Val | Leu | Tyr | Arg | Gly | Phe |
| | | | | 85 | | | | | 90 | | | | | 95 | |
| Lys | Asn | Glu | Cys | Pro | Ser | Gly | Ile | Val | Asn | Glu | Glu | Asn | Phe | Lys | Gln |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Ile | Tyr | Ser | Gln | Phe | Phe | Pro | Gln | Gly | Asp | Ser | Ser | Thr | Tyr | Ala | Thr |
| | | 115 | | | | | 120 | | | | | 125 | | | |
| Phe | Leu | Phe | Asn | Ala | Phe | Asp | Thr | Asn | His | Asp | Gly | Ser | Val | Ser | Phe |
| | 130 | | | | | 135 | | | | | 140 | | | | |
| Glu | Asp | Phe | Val | Ala | Gly | Leu | Ser | Val | Ile | Leu | Arg | Gly | Thr | Val | Asp |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 |
| Asp | Arg | Leu | Asn | Trp | Ala | Phe | Asn | Leu | Tyr | Asp | Leu | Asn | Lys | Asp | Gly |
| | | | | 165 | | | | | 170 | | | | 175 | | |
| Cys | Ile | Thr | Lys | Glu | Glu | Met | Leu | Asp | Ile | Met | Lys | Ser | Ile | Tyr | Asp |
| | | | 180 | | | | | 185 | | | | | 190 | | |
| Met | Met | Gly | Lys | Tyr | Thr | Tyr | Ile | Ala | Leu | Arg | Glu | Glu | Ala | Ile | Arg |
| | | 195 | | | | | 200 | | | | | 205 | | | |
| Glu | His | Val | Gln | Ser | Phe | Phe | Gln | Lys | Met | Asp | Arg | Asn | Lys | Asp | Gly |
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| Val | Val | Thr | Ile | Glu | Glu | Phe | Ile | Glu | Ser | Cys | Gln | Lys | Asp | Glu | Asn |
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 cgtcgccgg; ccaaggggg; ctggtgagc gcctattct ggcacccgg cgcctcttc 180
 cagggccag ggggaggg; ggggggggg ggc atg tgg ggt caa ggc aga aag 234
 Met Arg Gly Gln Gly Arg Lys
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 Glu Ser Leu Ser Glu Ser Arg Asp Leu Asp Gly Ser Tyr Asp Gln Leu
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 Thr Gly His Pro Pro Gly Pro Ser Lys Lys Ala Leu Lys Gln Arg Phe
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 Pro Glu Gly Leu Glu Gln Leu Gln Glu Gln Thr Lys Phe Thr Arg Arg
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<213> Rattus sp.

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| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Asp | Gly | Ser | Tyr | Asp | Gln | Leu | Thr | Gly | His | Pro | Pro | Gly | Pro | Ser | Lys |
| | | 20 | | | | | | 25 | | | | | 30 | | |
| Lys | Ala | Leu | Lys | Gln | Arg | Phe | Leu | Lys | Leu | Leu | Pro | Cys | Cys | Gly | Pro |
| | 35 | | | | | | 40 | | | | | 45 | | | |
| Gln | Ala | Leu | Pro | Ser | Val | Ser | Glu | Asn | Ser | Val | Glu | Asp | Glu | Phe | Glu |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Leu | Ser | Thr | Val | Cys | His | Arg | Pro | Glu | Gly | Leu | Glu | Gln | Leu | Gln | Glu |
| | 65 | | | | 70 | | | | | 75 | | | | 80 | |
| Gln | Thr | Lys | Phe | Thr | Arg | Arg | Glu | Leu | Gln | Val | Leu | Tyr | Arg | Gly | Phe |
| | | | 85 | | | | | | 90 | | | | | 95 | |
| Lys | Asn | Glu | Cys | Pro | Ser | Gly | Ile | Val | Asn | Glu | Glu | Asn | Phe | Lys | Gln |
| | 100 | | | | | | | 105 | | | | | 110 | | |
| Ile | Tyr | Ser | Gln | Phe | Phe | Pro | Gln | Gly | Asp | Ser | Ser | Asn | Tyr | Ala | Thr |
| | 115 | | | | | | 120 | | | | | 125 | | | |
| Phe | Leu | Phe | Asn | Ala | Phe | Asp | Thr | Asn | His | Asp | Gly | Ser | Val | Ser | Phe |
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| Gln | Asp | Phe | Val | Ala | Gly | Leu | Ser | Val | Ile | Leu | Arg | Gly | Thr | Ile | Asp |
| 145 | | | 150 | | | | | | 155 | | | | | 160 | |
| Asp | Arg | Leu | Ser | Tyr | Ala | Phe | Asn | Leu | Tyr | Asp | Leu | Asn | Lys | Asp | Gly |
| | 165 | | | | | | | | 170 | | | | 175 | | |
| Cys | Ile | Thr | Lys | Gln | Glu | Met | Leu | Asp | Ile | Met | Lys | Ser | Ile | Tyr | Asp |
| | 180 | | | | | | 185 | | | | | | 190 | | |
| Met | Met | Gly | Lys | Tyr | Thr | Tyr | Pro | Ala | Leu | Arg | Gln | Gln | Ala | Pro | Arg |
| | 195 | | | | | | 200 | | | | | 205 | | | |
| Gln | His | Val | Gln | Ser | Phe | Ile | Gln | Lys | Met | Asp | Arg | Asn | Lys | Asp | Gly |
| | 210 | | | | | 215 | | | | | 220 | | | | |

Val Val Thr Ile Ala Ala Ile Ile Ala Ser Cys Gln Ala Arg Ala Asn
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 Ser Val Asp Asp Glu Phe Glu Leu Ser Thr Val Cys His Arg Pro Glu
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cag gtc ctg tac cgg ggc ttc aag aac gaa tgt ccc agc gga att gtc 425
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aat gag gag aac ttc aag cag att tac ttc cag ttc ttc cct cca gga 473
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 75 80 85

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 125 130 135

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 Ser Cys Gln Lys Asp Glu Asn Ile Met Arg Ser Met Gln Leu Phe Asp
 205 210 215

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 Asn Val Ile
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atgtctaac cctagtccag ggggacctca cccctctctt cccaggtcta tctctctctt 966

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ggtgggggtg agaatagaa; ggcttgaca gattatgatt gctcaggcat accagttat 1446

agctccaaat tccacaggtt tgttctctt ggaatttaa attaaattt cagggtttg 1506

cagaagact tgtctcttga gaaatgctc agaatcttc caccctctc tgggtatcca 1566

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tctatgatt ggttgagga gtagtgag gatttggtt ggttgagct ttttgatg 1686

ctgcacaaat tctatctca cctctctt tcttggtt gtttgaggt ctatgattg 1746

agttctctt tctatggtt tctatagatt ttttggtt ctatctctt gtttgatg 1806

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 <211> Homo sapiens

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 Gln Thr Lys Phe Thr Arg Lys Glu Leu Gln Val Leu Tyr Arg Gly Phe
 50 55 60
 Lys Asn Glu Cys Pro Ser Gly Ile Val Asn Glu Glu Asn Phe Lys Gln
 65 70 75 80
 Ile Tyr Ser Gln Phe Phe Pro Gln Gly Asp Ser Ser Thr Tyr Ala Thr
 85 90 95
 Phe Leu Phe Asn Ala Phe Asp Thr Asn His Asp Gly Ser Val Ser Phe
 100 105 110
 Glu Asp Phe Val Ala Gly Leu Ser Val Ile Leu Arg Gly Thr Val Asp
 115 120 125
 Asp Arg Leu Asn Trp Ala Phe Asn Leu Tyr Asp Leu Asn Lys Asp Gly
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 Cys Ile Thr Lys Glu Glu Met Leu Asp Ile Met Lys Ser Ile Tyr Asp
 145 150 155 160
 Met Met Gly Lys Tyr Thr Tyr Pro Ala Leu Arg Glu Glu Ala Pro Arg
 165 170 175
 Glu His Val Glu Ser Phe Phe Gln Lys Met Asp Arg Asn Lys Asp Gly
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 Ile Met Arg Ser Met Gln Leu Phe Asp Asn Val Ile
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<220>
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[illegible]

[illegible]

- * 210 = 26
- * 211 = 210
- * 212 = 197
- * 213 = similar, see

• 400 • 20

Met Arg Gly Gln Gly Arg Lys Glu Ser Leu Ser Asp Ser Arg Asp Leu
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Asp Gly Ser Tyr Asp Glu Leu Thr Asp Ser Val Glu Asp His Thr Glu

Leu Ser Thr Val Cys His Arg Ile Glu Gly Leu Glu Gln Leu Glu His
 41 45
 Gln Thr Lys Ile Thr Arg Lys Glu Leu Gln Val Leu Tyr Arg Gly Phe
 51 55
 Lys Asn Glu Cys Pro Ser Gly Ile Val Asn Glu Glu Asn Ile Lys Gln
 61 65
 Ile Tyr Ser Gln Ile Phe Pro Gln Gly Asp Ser Ser Thr Tyr Ala Thr
 71 75
 Phe Leu Phe Asn Ala Phe Asp Thr Asn His Asp Gly Ser Val Ser Ile
 81 85
 Glu Asp Phe Val Ala Gly Leu Ser Val Ile Leu Arg Gly Thr Val Asp
 91 95
 Asp Arg Leu Asn Trp Ala Phe Asn Leu Tyr Asp Leu Asn Lys Asp Gly
 101 105
 Cys Ile Thr Lys Glu Glu Met Leu Asp Ile Met Lys Ser Ile Tyr Asp
 111 115
 Met Met Gly Lys Tyr Thr Tyr Pro Ala Leu Arg Glu Glu Ala Pro Arg
 121 125
 Glu His Val Glu Asn Phe Phe Gln Lys Met Asp Arg Asn Lys Asp Gly
 131 135
 Val Val Thr Ile Glu Glu Phe Ile Glu Ser Cys Gln Lys Asp Glu Asn
 141 145
 Ile Met Arg Ser Met Gln Leu Phe Asp Asn Val Ile
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<210> 27

<211> 2057

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<213> Simian sp.

<220>

<221> CDS

<222> (208)...(363)

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 ggttgcgtt tttgtgacaa ggttgcgtt tttgtgacaa ggttgcgtt tttgtgacaa 180
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 Met Arg Gly Gln Gly Arg Lys Glu Ser
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[illegible]

Val Thr Lys Ile Thr Arg Arg Val Leu Ala Val Leu Tyr Arg Gly Ile
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 Lys Asn Glu Cys Pro Ser Gly Ile Val Asn Glu Glu Asn Ile Lys Glu
 115 120 125
 Ile Tyr Ser Ala Phe Phe Pro Val Gly Asp Ser Ser Asn Tyr Ala Thr
 130 135 140
 Phe Leu Ile Asn Ala Phe Asp Thr Asn His Asp Gly Ser Val Ser Phe
 145 150 155
 Glu Asp Ile Val Ala Gly Leu Ser Val Ile Leu Arg Gly Thr Ile Asp
 160 165 170
 Asp Arg Leu Ser Trp Ala Phe Asn Leu Tyr Asp Leu Asn Lys Asp Gly
 175 180 185
 Cys Ile Thr Lys Gln Glu Met Leu Asp Ile Met Lys Ser Ile Tyr Asp
 190 195 200
 Met Met Gly Lys Tyr Thr Tyr Pro Ala Leu Arg Glu Glu Ala Pro Arg
 205 210 215
 Glu His Val Glu Ser Phe Phe Gln Lys Met Asp Arg Asn Lys Asp Gly
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 Ile Met Arg Ser Met Gln Leu Ser Pro Leu Leu Asn
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<210> 29

<211> 1904

<212> DNA

<213> Rattus sp.

<220>

<221> CDS

<222> (1)...(675)

<400> 29

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 1 5 10 15
 cga tat cct tac cag tgg gta att ggg ttg ctg ttg cca gac agc gta 96
 Arg Ser Leu Tyr Gln Leu Val Thr Gly Ser Leu Ser Pro Asp Ser Val
 20 25 30
 gag gat tat ttt gaa tta taa aag ata tgg taa taa cct tat ttt cta 144
 Glu Asp Glu Phe Glu Leu Ser Thr Val Cys His Arg Pro Glu Gly Leu
 35 40 45
 taa caa tta tat gaa cct att att tta aca ttt aat gaa tta cag tta 192
 Glu Gln Leu Val Glu Glu Val Thr Lys Phe Thr Arg Arg Glu Leu Gln Val
 50 55 60

141
 Ser Tyr Arg Gly Ile Lys Asn Glu Cys Leu Ser Gly Ile Val Asn Glu
 147

149
 Glu Asn Phe Lys Gln Ile Tyr Ser Gln Phe Phe Pro Gln Gly Asp Ser
 155 161 167

170
 Ser Asn Tyr Ala Thr Phe Leu Ile Asn Ala Phe Asp Thr Asn His Asp
 176 182 188

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 Gly Ser Val Ser Phe Glu Asp Phe Val Ala Gly Leu Ser Val Ile Leu
 197 203 209

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 Arg Gly Thr Ile Asp Asp Arg Leu Ser Trp Ala Phe Asn Leu Tyr Asp
 218 224 230

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 Leu Asn Lys Asp Gly Cys Ile Thr Lys Glu Glu Met Leu Asp Ile Met
 239 245 251 257

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 Lys Ser Ile Tyr Asp Met Met Gly Lys Tyr Thr Tyr Pro Ala Leu Arg
 266 272 278

281
 Glu Glu Ala Pro Arg Glu His Val Glu Ser Phe Phe Gln Lys Met Asp
 287 293 299

302
 Arg Asn Lys Asp Gly Val Val Thr Ile Glu Glu Phe Ile Glu Ser Cys
 308 314 320

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 Gln Gln Asp Glu Asn Ile Met Arg Ser Met Gln Leu Phe Asp Asn Val
 329 335 341

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Glu Asp Gln Phe Glu Leu Ser Thr Val Cys His Arg Pro Gln Gly Leu
          35          40          45
Glu Gln Leu Gln Glu Gln Thr Lys Phe Thr Arg Arg Glu Leu Gln Val
          50          55          60
Leu Tyr Arg Gly Phe Lys Asn Glu Cys Pro Ser Gly Ile Val Asn Glu
          65          70          75          80
Glu Asn Phe Lys Gln Ile Tyr Ser Gln Phe Phe Pro Gln Gly Asp Ser
          85          90          95
Ser Asn Tyr Ala Thr Phe Leu Phe Asn Ala Phe Asp Thr Asn His Asp
          100          105          110
Gly Ser Val Ser Phe Gln Asp Phe Val Ala Gly Leu Ser Val Ile Leu
          115          120          125
Arg Gly Thr Ile Asp Asp Arg Leu Ser Trp Ala Phe Asn Leu Tyr Asp
          130          135          140
Leu Asn Lys Asp Gly Cys Ile Thr Lys Glu Glu Met Leu Asp Ile Met
          145          150          155          160

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|----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| <400> 31 | | | | | | | | | | | | | | | | | |
| atg | cag | ccg | ggt | aag | gaa | gtg | aca | aag | ggg | tgg | gac | ggc | agc | ctc | ctg | 46 | |
| Met | Gln | Pro | Ala | Lys | Glu | Val | Thr | Lys | Ala | Ser | Asp | Gly | Ser | Leu | Leu | | |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | | | |
| | | | | | | | | | | | | | | | | | |
| ggg | gac | ctc | ggy | cac | aca | cca | ctt | agc | aag | aag | gag | ggg | atc | aag | tgg | 96 | |
| Gly | Asp | Leu | Gly | His | Thr | Pro | Leu | Ser | Lys | Lys | Glu | Gly | Ile | Lys | Trp | | |
| | | 20 | | | | | | 25 | | | | | 30 | | | | |
| | | | | | | | | | | | | | | | | | |
| cag | agg | ccg | agg | ctc | agc | cgc | cag | ggt | tgg | atg | aga | tgc | tgc | ctg | gtc | 144 | |
| Gln | Arg | Pro | Arg | Leu | Ser | Arg | Gln | Ala | Leu | Met | Arg | Cys | Cys | Leu | Val | | |
| | 35 | | | | | | 40 | | | | | 45 | | | | | |
| | | | | | | | | | | | | | | | | | |
| aag | tgg | atc | ctg | tcc | agc | aca | ggc | cca | cag | ggc | tca | gat | agc | agc | gac | 192 | |
| Lys | Trp | Ile | Leu | Ser | Ser | Thr | Ala | Pro | Gln | Gly | Ser | Asp | Ser | Ser | Asp | | |
| | 50 | | | | | 55 | | | | | 60 | | | | | | |
| | | | | | | | | | | | | | | | | | |
| agc | gag | ctc | tgg | ctg | tcc | acc | ggc | cgc | tac | cag | cca | tgc | ttg | ctg | gac | 240 | |
| Ser | Glu | Leu | Glu | Leu | Ser | Thr | Val | Arg | His | Gln | Pro | Glu | Gly | Leu | Asp | | |
| 65 | | | | 70 | | | | 75 | | | | | | 80 | | | |
| | | | | | | | | | | | | | | | | | |
| tgg | ctg | cag | ggt | cag | att | aag | tcc | atc | aag | aag | tgc | tgc | cag | tcc | ctc | 288 | |
| Gln | Leu | Gln | Ala | Gln | Thr | Lys | Phe | Thr | Lys | Lys | Glu | Leu | Gln | Ser | Leu | | |
| | | | 85 | | | | 90 | | | | | | 95 | | | | |
| | | | | | | | | | | | | | | | | | |
| tat | agg | ttc | ttc | agg | att | tgc | tgc | ctc | agg | ttc | tgc | tgc | ttc | gaa | gac | 336 | |
| Tyr | Arg | Gly | Phe | Lys | Asn | Glu | Cys | Pro | Thr | Gly | Leu | Val | Asp | Glu | Asp | | |
| | | 100 | | | | | 105 | | | | | | 110 | | | | |
| | | | | | | | | | | | | | | | | | |
| acc | tcc | aaa | ctc | att | tac | ggg | cag | tcc | tcc | ctc | cag | tgc | ttc | ttc | acc | 384 | |
| Thr | Phe | Lys | Leu | Ile | Tyr | Ala | Gln | Phe | Phe | Pro | Gln | Gly | Asp | Ala | Thr | | |
| | | 115 | | | | | 120 | | | | | 125 | | | | | |
| | | | | | | | | | | | | | | | | | |
| acc | tac | tca | cac | tcc | tcc | tcc | acc | gac | tcc | tac | tgc | tgc | ttc | ttc | ttg | 432 | |
| Thr | Tyr | Ala | His | Phe | Leu | Ile | Asn | Ala | Ile | Asp | Ala | Asp | Gly | Asn | Gly | | |
| | 130 | | | | | 135 | | | | | 140 | | | | | | |

acg atc cag ttt gag gag ttt gtt gtt ttt ctc atc atg atg ggg 480
 Ala Ile His Phe Glu Asp Phe Val Val Gly Leu Ser Ile Leu Leu Arg
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ggt aia gtr cag gag aag ctc aag tgg gtc ttt aat ctc tac gag att 520
 Gly Thr Val His Glu Lys Leu Lys Trp Ala Phe Asn Leu Tyr Asp Ile
 165 170 175

aac aag gat ggt tac atc acc aaa gag gag atg ctg gcc atc atg aag 576
 Asn Lys Asp Gly Tyr Ile Thr Lys Glu Glu Met Leu Ala Ile Met Lys
 180 185 190

tcc atc tat gac atg atg ggc cgc cac acc tac ccc atc ctg cgg gag 624
 Ser Ile Tyr Asp Met Met Gly Arg His Thr Tyr Pro Ile Leu Arg Glu
 195 200 205

gac ggc cgg ggc gag cac gtg gag agg ttc ttc gag aaa atg gac cgg 672
 Asp Ala Pro Ala Glu His Val Glu Arg Phe Phe Glu Lys Met Asp Arg
 210 215 220

aac cag gat ggg gta gtg acc att gaa gag ttc ctg gag gcc tgt cag 720
 Asn Gln Asp Gly Val Val Thr Ile Glu Glu Phe Leu Glu Ala Cys Gln
 225 230 235 240

aag gat gag aac atc atg agc tcc atg cag ctg ttt gag aat gtc atc 768
 Lys Asp Glu Asn Ile Met Ser Ser Met Gln Leu Phe Glu Asn Val Ile
 245 250 255

taggacacgt ccaaaggagt gcatggccac agccacctcc accccaaga aacctccatc 828

ctgccaggag cagcctccaa gaaactttta aaaaatagat ttgcaaaaag tgaacagatt 888

gotacacaca cacacacaca cacacacaca cacacacaca cacagccatt catctgggct 948

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caggtctgca ggcaccagc tgctggatgt caccagaag gggctcgagt gccctgcag 1128

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tggtttgta cctccctc agcacagat ctctctta agtccctt agttcagg 1668

agaaagtgg ttacagagct ggcagccag gggggggg cagagctca agtcttgg 1728

gaaggggggt ggaatgggtt gggggggg gggggggg gggggggg 178
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 gggggggg gggggggg gggggggg gggggggg gggggggg 284

<210> 32

 $\langle 211 \rangle = 256$

CONCLUSIONS

0213- Homo sapiens

493-32

Met Gln Pro Ala Lys Gln Val Thr Lys Ala Ser Asp Gly Ser Leu Leu

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$\frac{1}{2}$ $\frac{1}{2}$
 $\frac{1}{2}$ $\frac{1}{2}$

Gly Asp Leu Phe His Thr Pro Leu Ser Lys Lys Glu Gly Ile Lys Trp

22

44

31

Gln Arg Pro Arg Leu Ser Ala Gln Ala Leu Met Arg Cys Cys Leu Val

31.

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Lys Trp Ile Leu Ser Ser Thr Ala Pro Gln Gly Ser Asp Ser Ser Asp

157

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Mon Tue Wed Thu Fri Sat Sun Mon Tue Wed Thu Fri Sat Sun

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Gln Leu Gln Ala Gln Thr Lys Phe Thr Lys Lys Glu Leu Gln Ser Leu
 85 90 95

Tyr Arg Gly Phe Lys Asn Gln Cys Ile Thr Gly Leu Val Arg Gln Arg
 100 105 110

Thr Phe Lys Leu Ile Tyr Ala Gln Phe Phe Pro Gln Gly Asp Ala Thr
 115 120 125

Thr Tyr Ala His Phe Leu Phe Asn Ala Phe Asp Ala Asp Gly Asn Gly
 130 135 140

Ala Ile His Phe Glu Asp Phe Val Val Gly Leu Ser Ile Leu Leu Arg
 145 150 155 160

Gly Thr Val His Glu Lys Leu Lys Trp Ala Phe Asn Leu Tyr Asp Ile
 165 170 175

Asn Lys Asp Gly Tyr Ile Thr Lys Glu Glu Met Leu Ala Ile Met Lys
 180 185 190

Ser Ile Tyr Asp Met Met Gly Arg His Thr Tyr Pro Ile Leu Arg Glu
 195 200 205

Asp Ala Pro Ala Glu His Val Glu Arg Phe Phe Glu Lys Met Asp Arg
 210 215 220

Asn Gln Asp Gly Val Val Thr Ile Glu Glu Phe Leu Glu Ala Cys Gln
 225 230 235 240

Lys Asp Glu Asn Ile Met Ser Ser Met Gln Leu Phe Glu Asn Val Ile
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cat gag aag ctc aag tgg gcc ttc aat ctc tac gac atc aac aag gac 96
 His Glu Lys Leu Lys Trp Ala Phe Asn Leu Tyr Asp Ile Asn Lys Asp
 20 25 30

ggt tac atc acc aaa cag gag atg ctg gac atc atg aat tcc atc tac 144
 Gly Tyr Ile Thr Lys Glu Glu Met Leu Ala Ile Met Lys Ser Ile Tyr
 35 40 45

gac atg atg ggt ggt cag acc tcc ctt atc ctg ggt gag gac gac ctt 192
 Asp Met Met Gly Arg His Thr Tyr Pro Ile Leu Arg Glu Asp Ala Pro
 50 55 60

14
 Leu Glu His Val Gln Arg Ile Ile Gln Lys Met Arg Arg Asn Val Arg
 65 70 75 80

85 90 95
 Gly Val Val Thr Ile Asp Glu Phe Leu Thr Cys Gln Lys Asp Gln

100 105
 Asn Ile Met Ser Ser Met Gln Leu Ile Gln Asn Val Ile

397

442

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Gly Tyr Ile Thr Lys Glu Glu Met Leu Ala Ile Met Lys Ser Ile Tyr
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Asp Met Met Gly Arg His Thr Tyr Pro Ile Leu Arg Glu Asp Ala Pro
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Leu Glu His Val Glu Arg Phe Phe Gln Lys Met Asp Arg Asn Gln Asp
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Gly Val Val Thr Ile Asp Glu Phe Leu Glu Thr Cys Gln Lys Asp Glu
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Asn Ile Met Ser Ser Met Gln Leu Phe Glu Asn Val Ile
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<210> 37

<211> 131

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<213> Homo sapiens

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<221> CDS

<222> (1)..(336)

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<223> At position 495, n=any amino acid

<400> 37

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ggc ggt ttc ctg tac gct cag aac agc acc aag cgc agc att aaa gag      96
Gly Gly Phe Leu Tyr Ala Gln Asn Ser Thr Lys Arg Ser Ile Lys Glu
          20             25             30

cgg ctg atg aag ctg ttg ccc tgc tca gct gcc aaa acg tgg tct cct     144
Arg Leu Met Lys Leu Leu Pro Cys Ser Ala Ala Lys Thr Ser Ser Pro
          35             40             45

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Phe Phe Leu Thr Leu Pro Ser His Asn Ser Gln Arg Ser Ile Glu Lys
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1. *Journal of the American Medical Association*, 1997; 277: 103-107.

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 1040 1

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Glu His Val Glu Ser Phe Phe Gln Lys Met Asp Arg Asn Lys Asp Gly
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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
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 Leu Leu His Leu Leu Gly Leu Ile Asp Phe Ser Glu Asp Ser Val Glu
 30 35 40

gat gaa ctg gag atg gac aat ggt agt cat ctg ctt gag gac ctt gag 435
 Asp Glu Leu Glu Met Ala Thr Val Arg His Arg Pro Glu Ala Leu Glu
 45 50 55

ctt ctg gaa gac cat aac aaa ttt aat aag aag gag ctt cag aat ctt 483
 Leu Leu Glu Ala Gln Ser Lys Phe Thr Lys Lys Glu Leu Gln Ile Leu
 60 65 70

tac aga gga ttt aag aac gaa tgc ccc agt ggt ctt gtt aat gaa gaa 531
 Tyr Arg Gly Phe Lys Asn Glu Cys Pro Ser Gly Val Val Asn Gln Glu
 75 80 85

aat ttc aaa gag att tat tgg cag ttc ttc ttc ttc gga gag ttc aat 579
 Thr Phe Lys Glu Ile Tyr Ser Gln Phe Phe Pro Gln Gly Asp Ser Thr
 90 95 100 105

ata tat gca cat ttt ctg ttc aat ggt ttc gat agc gac cac aat ggt 627
 Thr Tyr Ala His Phe Leu Phe Asn Ala Phe Asp Thr Asp His Asn Gly
 110 115 120

ptt ptt ggt ttt ggt ggt ttt aat aat aat aat aat aat aat aat 675
 Ala Val Ser Phe Gln Asp Phe Ile Lys Gly Leu Ser Ile Leu Leu Arg
 125 130 135

ggt ata gta ttc ttc ttc ttc aat ttc ggt ttc aat ctg tat tat ata 723
 Gly Thr Val Phe Phe Lys Leu Asn Thr Ala Phe Asn Leu Tyr Asp Ile
 140 145 150

aat aat ggt ttt ttt aat aat aat aat aat aat aat aat aat aat 771
 Asn Lys Asp Gly Tyr Ile Thr Lys Glu Glu Met Leu Asp Ile Met Lys
 155 160 165

aca aca taa taa atg aca aca aca tgc aca taa aca taa aca aca aca 914
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189 190 191 192 193 194 195 196 197 198 199 200

gta taa taa taa taa taa taa taa taa taa taa taa taa taa taa taa 915
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215 216 217 218 219 220 221 222 223 224 225 226 227 228

aaa gat taa taa taa atg gaa taa atg gaa taa taa taa gaa aca taa att 917
Lys Asp Glu Asn Ile Met Arg Ser Met Gln Leu Phe Glu Asn Val Ile
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caatgata caatgata aattttta atgttttc aatttttc aatttttc 2223

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Met Leu Thr Leu Glu Trp Gln Ser Glu Gly Leu Gln Thr Val Gly Ile
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 Val Val Ile Ile Cys Ala Ser Leu Lys Leu Leu His Leu Leu Gly Leu
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 Ile Asp Phe Ser Glu Asp Ser Val Glu Asp Glu Leu Glu Met Ala Thr
 35 40 45
 Val Arg His Arg Pro Glu Ala Leu Glu Leu Leu Glu Ala Gln Ser Lys
 50 55 60
 Phe Thr Lys Lys Glu Leu Gln Ile Leu Tyr Arg Gly Phe Lys Asn Glu
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 Cys Pro Ser Gly Val Val Asn Glu Glu Thr Phe Lys Glu Ile Tyr Ser
 85 90 95
 Gln Phe Phe Pro Gln Gly Asp Ser Thr Thr Tyr Ala His Phe Leu Phe
 100 105 110
 Asn Ala Phe Asp Thr Asp His Asn Gly Ala Val Ser Phe Glu Asp Phe
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 145 150 155 160
 Lys Glu Glu Met Leu Asp Ile Met Lys Ala Ile Tyr Asp Met Met Gly
 165 170 175
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 Glu Thr Phe Phe Gln Lys Met Asp Lys Asn Lys Asp Gly Val Val Thr
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 Val Arg His Arg Pro Glu Ala Leu Glu Leu Leu Glu Ala Gln Ser Lys
 50 55 60
 Phe Thr Lys Lys Glu Leu Gln Ile Leu Tyr Arg Gly Phe Lys Asn Glu
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 Cys Pro Ser Gly Val Val Asn Glu Glu Thr Phe Lys Glu Ile Tyr Ser
 85 90 95
 Gln Phe Phe Pro Gln Gly Asp Ser Thr Thr Tyr Ala His Phe Leu Phe
 100 105 110
 Asn Ala Phe Asp Thr Asp His Asn Gly Ala Val Ser Phe Glu Asp Phe
 115 120 125
 Ile Lys Gly Leu Ser Ile Leu Leu Arg Gly Thr Val Gln Glu Lys Leu
 130 135 140
 Asn Trp Ala Phe Asn Leu Tyr Asp Ile Asn Lys Asp Gly Tyr Ile Thr
 145 150 155 160
 Lys Glu Glu Met Leu Asp Ile Met Lys Ala Ile Tyr Asp Met Met Gly
 165 170 175
 Lys Cys Thr Tyr Pro Val Leu Lys Glu Asp Ala Pro Arg Gln His Val
 180 185 190
 Glu Thr Phe Phe Gln Lys Met Asp Lys Asn Lys Asp Gly Val Val Thr
 195 200 205
 Ile Asp Gln Phe Ile Glu Ser Cys Gln Lys Asp Glu Asn Ile Met Arg
 210 215 220
 Ser Met Gln Leu Phe Glu Asn Val Ile
 225 230

Keywords: children's literature; reading; literacy; school; teacher education

+ 120 >
 + 121 > 0102
 + 122 > 0103...0103

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 Met Leu Thr Leu Ala Trp Ala Ser Glu
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Gly Leu Gln Thr Val Gly Ile Val Val Ile Ile Cys Ala Ser Leu Lys
10 15 20 25

ctg ctt cat ttg ctg gga ctg att gat ttt tgg gaa gac agc gtg gaa 387
Leu Leu His Leu Leu Gly Leu Ile Asp Phe Ser Glu Asp Ser Val Glu
30 35 40

gat gaa ggg gag atg ggc aac ggc agc cat ggg gct gag gcc gct gag 435
Asp Glu Leu Glu Met Ala Thr Val Arg His Arg Pro Glu Ala Leu Glu
45 50 55

Att ctg gaa gag cag agc aaa ttt att aag aaq cgt cag atc ctt 483
Leu Leu Gln Ala Gln Ser Lys Phe Thr Lys Lys Glu Leu Gln Ile Leu

64 65 70

tac aga gga ttt aag aac gaa tgc ccc agt ggt gtt gtt aat gaa gaa 531
 Tyr Arg Gly Phe Lys Asn Glu Cys Pro Ser Gly Val Val Asn Glu Glu
 75 80 85

Met His Arg Gly Ala Leu Met Arg Val Thr Met Met Ser Arg Gly Val Met Ala 479
 Thr Phe Lys Glu Ile Tyr Ser Gln Ile Phe Pro Gln Gly Asp Ser Thr
 90 95 100 105

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Ala Val Ser His Glu Asp Thr Ile Lys Gly Leu Ser Ile Leu Leu Arg
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| 2001 | 52 |
| 2002 | 53 |
| 2003 | 54 |

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 Phe Thr Lys Lys Glu Leu Gln Ile Leu Tyr Arg Gly Phe Lys Asn Gln
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 Cys Pro Ser Gly Val Val Asn Glu Glu Thr Phe Lys Glu Ile Tyr Ser
 85 90 95
 Gln Phe Phe Pro Gln Gly Asp Ser Thr Thr Tyr Ala His Phe Leu Phe
 100 105 110
 Asn Ala Phe Asp Thr Asp His Asn Gly Ala Val Ser Phe Glu Asp Phe
 115 120 125
 Ile Lys Gly Leu Ser Ile Leu Leu Arg Gly Thr Val Gln Glu Lys Leu
 130 135 140
 Asn Trp Ala Phe Asn Leu Tyr Asp Ile Asn Lys Asp Gly Tyr Ile Thr
 145 150 155 160
 Lys Glu Glu Met Leu Asp Ile Met Lys Ala Ile Tyr Asp Met Met Gly
 165 170 175
 Lys Cys Thr Tyr Pro Val Leu Lys Glu Asp Ala Pro Arg Gln His Val
 180 185 190
 Glu Thr Phe Phe Gln Ala Val Phe His Cys Ile Ile Lys Trp Lys Phe
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Met Asn Gly Val Glu Gly Asn Asn Glu

1

5

ctc cct ctc ggt aac acc tag acc tcc gcc ctt gtc ccg gaa gat ctg 159

Leu Pro Leu Ala Asn Thr Ser Thr Ser Ala Leu Val Pro Glu Asp Leu

10

15

20

25

tat ctg aag caa gac tgg tgg ctg agt gag gaa act gac arg gtc ccg 207

Asp Leu Lys Gln Asp Gln Pro Leu Ser Glu Glu Thr Asp Thr Val Arg

30

35

40

| | |
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 Glu Met Glu Ala Ala Gly Glu Ala Gly Ala Glu Gly Gly Ala Ser Pro
 45 50 55 </p> | 455 |
| <p> gat tgg aag caa ttt gag cta cag cta ttt ctc aga atg aat gaa aat
 Asp Ser Glu His Cys Asp Pro Gln Leu Cys Leu Arg Val Ala Glu Asn
 60 65 70 </p> | 463 |
| <p> gag tgt ggt ggc gca ggg gga gag ggg ctg gag gat ggt atg ttt tca
 Gly Cys Ala Ala Ala Ala Gly Glu Gly Leu Glu Asp Gly Leu Ser Ser
 75 80 85 </p> | 351 |
| <p> tca aag tgt ggg gac gca ccc ttg ggg tct gtg gca gcc aac gac agc
 Ser Lys Cys Gly Asp Ala Pro Leu Ala Ser Val Ala Ala Asn Asp Ser
 90 95 100 105 </p> | 399 |
| <p> aat aaa aat ggc tgt cag ctt gca ggg ccg ctc agc cct gct aag cca
 Asn Lys Asn Gly Cys Gln Leu Ala Gly Pro Leu Ser Pro Ala Lys Pro
 110 115 120 </p> | 447 |
| <p> aaa act ctg gaa gcc agt ggt gca gtg ggc ctg ggg tgg cag atg atg
 Lys Thr Leu Glu Ala Ser Gly Ala Val Gly Leu Gly Ser Gln Met Met
 125 130 135 </p> | 495 |
| <p> cca ggg ccg aag aag acc aag gta atg act acc aag ggc gcc atc tct
 Pro Gly Pro Lys Lys Thr Lys Val Met Thr Thr Lys Gly Ala Ile Ser
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| <p> gcg act aca ggc aag gaa gga gaa gca ggg gcg gca atg cag gaa aag
 Ala Thr Thr Gly Lys Glu Gly Glu Ala Gly Ala Ala Met Gln Glu Lys
 155 160 165 </p> | 591 |
| <p> aag ggg gtg cag aaa gaa aaa aag gca gct gga gga ggg aaa gac gag
 Lys Gly Val Gln Lys Glu Lys Lys Ala Ala Gly Gly Gly Lys Asp Glu
 170 175 180 185 </p> | 639 |
| <p> act cgt cct aga gcc cct aag atc aat aac tgc atg gac tcc ctg gaa
 Thr Arg Pro Arg Ala Pro Lys Ile Asn Asn Cys Met Asp Ser Leu Glu
 190 195 200 </p> | 687 |
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 Ala Ile Asp Gln Glu Leu Ser Asn Val Asn Ala Gln Ala Asp Arg Ala
 205 210 215 </p> | 735 |
| <p> ttc ctc cag ctg gaa cgc aaa ttt ggg cgg atg aga agg ctc cac atg
 Phe Leu Gln Leu Glu Arg Lys Phe Gly Arg Met Arg Arg Leu His Met
 220 225 230 </p> | 783 |
| <p> cag cgc cga agt ttc atc atc caa aac atc cca ggt ttc tgg gtc aca
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| <p> taa gag atg atg agt taa atc atc aat tta gag gta gag gag ttt aag
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 270 275 280 </p> | 927 |

111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130
 His Ile Arg Ala Gly Tyr Lys Ile Lys Phe Ile Ile Gln Ser Asn Ile
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140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159
 Tyr Ile Arg Asn Gln Gly Leu Val Lys Gln Tyr Gln Arg Arg Ser Ser
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180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199
 Gly Arg Val Val Ser Leu Ser Thr Pro Ile Arg Trp His Arg Gly Gln
 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219

220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239
 Gln Pro Gln Ala His Ile His Arg Asn Arg Gln Gly Asn Thr Ile Pro
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260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279
 Ser Phe Phe Asn Trp Phe Ser Asp His Ser Leu Leu Gln Phe Asp Arg
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300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319
 Ile Ala Gln Ile Ile Lys Gly Glu Leu Trp Ser Asn Pro Leu Gln Tyr
 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339

340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359
 Tyr Leu Met Gly Asp Gly Pro Arg Arg Gly Val Arg Val Pro Pro Arg
 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379

380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399
 Gln Pro Val Gln Ser Pro Arg Ser Phe Arg Phe Gln Ser Gly
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420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439
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 35 40 45

Ala Gly Ala Glu Gly Gly Ala Ser Pro Asp Ser Glu His Cys Asp Pro
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Gln Leu Cys Leu Arg Val Ala Glu Asn Gly Cys Ala Ala Ala Ala Gly
 65 70 75 80

Glu Gly Leu Glu Asp Gly Leu Ser Ser Ser Lys Cys Gly Asp Ala Pro
 85 90 95

Leu Ala Ser Val Ala Ala Asn Asp Ser Asn Lys Asn Gly Cys Gln Leu
 100 105 110

Ala Gly Pro Leu Ser Pro Ala Lys Pro Lys Thr Leu Glu Ala Ser Gly
 115 120 125

Ala Val Gly Leu Gly Ser Gln Met Met Pro Gly Pro Lys Lys Thr Lys
 130 135 140

Val Met Thr Thr Lys Gly Ala Ile Ser Ala Thr Thr Gly Lys Glu Gly
 145 150 155 160

Glu Ala Gly Ala Ala Met Gln Glu Lys Lys Gly Val Gln Lys Glu Lys
 165 170 175

Lys Ala Ala Gly Gly Gly Lys Asp Glu Thr Arg Pro Arg Ala Pro Lys
 180 185 190

Ile Asn Asn Cys Met Asp Ser Leu Glu Ala Ile Asp Gln Glu Leu Ser
 195 200 205

Asn Val Asn Ala Gln Ala Asp Arg Ala Phe Leu Gln Leu Glu Arg Lys
 210 215 220

Phe Gly Arg Met Arg Arg Leu His Met Gln Arg Arg Ser Phe Ile Ile
 225 230 235 240

Gln Asn Ile Pro Gly Phe Trp Val Thr Ala Phe Arg Asn His Pro Gln
 245 250 255

Leu Ser Pro Met Ile Ser Gly Gln Asp Glu Asp Met Met Arg Tyr Met
 260 265 270

Ile Asn Leu Glu Val Glu Glu Leu Lys His Pro Arg Ala Gly Cys Lys
 275 280 285

His Lys His Ile His Gln Ser Asn Ile Tyr His Arg Asn Gln Gly Leu
 21 24 27 30 33 36 39 42 45 48 51 54 57 60

Val Lys His Tyr His Arg Arg Ser Ser Gly Arg Val Val Ser Leu Ser
 63 66 69 72 75 78 81 84 87 90 93 96 99 102

Thr Pro Ile Arg Trp His Arg Gly Gln Gln Ile Gln Ala His Ile His
 105 108 111 114 117 120 123 126 129 132 135 138 141 144

Arg Asn Arg Gln Gly Asn Thr Ile Pro Ser His Phe Asn Trp Phe Ser
 147 150 153 156 159 162 165 168 171 174 177 180 183 186

Asp His Ser Leu Leu His Phe Asp Arg Ile Ala Gln Ile Ile Lys Gly
 189 192 195 198 201 204 207 210 213 216 219 222 225 228

Gln Leu Trp Ser Asn Pro Leu Gln Tyr Tyr Leu Met Gly Asp Gly Pro
 231 234 237 240 243 246 249 252 255 258 261 264 267 270

Arg Arg Gly Val Arg Val Pro Pro Arg Gln Pro Val Gln Ser Pro Arg
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<221> CDS

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 Gly Asp Pro Asp Leu Asp Gln Cys Gln Gly Leu Arg Gln Gln Thr Gln
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 Ala Thr Gln Val Met Ala Asn Thr Gly Gly Gly Ser Leu His Thr Val
 45 50 55

gtt gat tta ttg gaa ttt caa tat cct tta ttg ttt gtt ctt ttg ctt 306
 Ala Gln Gly Gly Ala Ser Gln Asp Pro Val Asp Cys Gly Ile Ala Leu
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| | |
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Gln Glu Asp Ala Pro Pro Ser Thr Lys Gly Leu Glu Ala Ala Ser Ala
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Ala Glu Ala Ala Asp Ser Ser Gln Lys Asn Gly Cys Gln Leu Gly Glu
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Pro Arg Gly Pro Ala Gly Gln Lys Ala Leu Glu Ala Cys Gly Ala Gly
125 130 135 | 498 |
| ggc ttg ggg tct cag atg ata ccg ggg aag aag gcc aag gaa gtg acg
Gly Leu Gly Ser Gln Met Ile Pro Gly Lys Lys Ala Lys Glu Val Thr
140 145 150 | 546 |
| act aaa aaa cgc gcc atc tcg gca gca gtg gaa aag gag gga gaa gca
Thr Lys Lys Arg Ala Ile Ser Ala Ala Val Glu Lys Glu Gly Glu Ala
155 160 165 | 594 |
| ggg gcg gcg atg gag gaa aag aag gta gtg cag aag gaa aaa aag gtg
Gly Ala Ala Met Glu Glu Lys Lys Val Val Gln Lys Glu Lys Lys Val
170 175 180 185 | 642 |
| gca gga ggg gtg aaa gag gag aca cgg ccc agg gcc ccg aag atc aat
Ala Gly Gly Val Lys Glu Glu Thr Arg Pro Arg Ala Pro Lys Ile Asn
190 195 200 | 690 |
| aac tgc atg gac tca ctg gag gcc atc gat caa gag ttg tca aac gta
Asn Cys Met Asp Ser Leu Glu Ala Ile Asp Gln Glu Leu Ser Asn Val
205 210 215 | 738 |
| aat gcc cag gct gac agg gcc ttc ctt cag ctt gag cgc aag ttt ggc
Asn Ala Gln Ala Asp Arg Ala Phe Leu Gln Leu Glu Arg Lys Phe Gly
220 225 230 | 786 |
| cgc atg cga agg ctc cac atg cag cgc aga agt ttc att atc cag aat
Arg Met Arg Arg Leu His Met Gln Arg Arg Ser Phe Ile Ile Gln Asn
235 240 245 | 834 |
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Ile Pro Gly Phe Trp Val Thr Ala Phe Arg Asn His Pro Gln Leu Ser
250 255 260 265 | 882 |
| cct atg atc agt ggc caa gat gaa gac atg ctg agg tac atg atc aat
Pro Met Ile Ser Gly Gln Asp Glu Asp Met Leu Arg Tyr Met Ile Asn
270 275 280 | 930 |
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Leu Glu Val Glu Glu Leu Lys His Pro Arg Ala Gly Cys Lys Phe Lys
285 290 295 | 978 |
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Phe Ile Phe Gln Gly Asn Pro Tyr Phe Arg Asn Glu Gly Leu Val Lys
300 305 310 | 1026 |

gaa tat gaa cag aga tcc ttt ggg cgg tgg gta tat ctc tcc att cca 1074
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 315 321 328
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 Ile Arg Trp His Arg Gly Gln Asp Pro Gln Ala His Ile His Arg Asn
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 Arg Glu Gly Asn Thr Ile Pro Ser Phe Phe Asn Trp Phe Ser Asp His
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 Trp Pro Asn Pro Leu Gln Tyr Tyr Leu Met Gly Glu Gly Pro Arg Arg
 380 385 390
 gga att cga ggc cca cca agg cag cca gtg gag agc gcc aga tcc ttc 1314
 Gly Ile Arg Gly Pro Pro Arg Gln Pro Val Glu Ser Ala Arg Ser Phe
 395 400 405
 agg ttc cag tct ggc taatctctgt cctgtgagaa gcttctgcac aagtttcctt 1369
 Arg Phe Gln Ser Gly
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 accacctcct ctgggacctt tgcttggcca acagcatgca gtcttcacac tgctttctct 1429
 tcatactgtg gattatcttt tcttttggtt ctaaatcttc agtaatcggg tgcaagattg 1489
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 tgggttatct atagaacaag ctgggtggctg atgggtgaat gctaggcgtg actgaggtaa 1969
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 caaataaaa tcttaagt gaggaaatc ttatgggact tctcttctc atggtgtga 2329
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<212> FRT

<213> Homo sapiens

<400> 55

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Gly Leu Ala Ala Pro Asp His Ala Ser Gly Asp Pro Asp Leu Asp Gln
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Cys Gln Gly Leu Arg Glu Glu Thr Glu Ala Thr Gln Val Met Ala Asn
35 40 45

Thr Gly Gly Gly Ser Leu Glu Thr Val Ala Glu Gly Gly Ala Ser Gln
50 55 60

Asp Pro Val Asp Cys Gly Pro Ala Leu Arg Val Pro Val Ala Gly Ser
65 70 75 80

Arg Gly Gly Ala Ala Thr Lys Ala Gly Gln Glu Asp Ala Pro Pro Ser
85 90 95

Thr Lys Gly Leu Glu Ala Ala Ser Ala Ala Glu Ala Ala Asp Ser Ser
100 105 110

Gln Lys Asn Gly Cys Gln Leu Gly Glu Pro Arg Gly Pro Ala Gly Gln
115 120 125

Lys Ala Leu Glu Ala Cys Gly Ala Gly Gly Leu Gly Ser Gln Met Ile
130 135 140

Pro Gly Lys Lys Ala Lys Glu Val Thr Thr Lys Lys Arg Ala Ile Ser
145 150 155 160

Ala Ala Val Glu Lys Glu Gly Glu Ala Gly Ala Ala Met Glu Glu Lys
165 170 175

Lys Val Val Gln Lys Glu Lys Lys Val Ala Gly Gly Val Lys Glu Glu
180 185 190

Thr Arg Pro Arg Ala Pro Lys Ile Asn Asn Cys Met Asp Ser Leu Glu
195 200 205

Ala Ile Asp Gln Glu Leu Ser Asn Val Asn Ala Gln Ala Asp Arg Ala
210 215 220

Phe Leu Gln Leu Glu Arg Lys Phe Gly Arg Met Arg Arg Leu His Met
225 230 235 240

Gln Arg Arg Ser Phe Ile Ile Gln Asn Ile Pro Gly Phe Trp Val Thr
245 250 255

Ala Phe Arg Asn His Pro Gln Leu Ser Pro Met Ile Ser Gly Gln Asp
260 265 270

Glu Asp Met Leu Arg Tyr Met Ile Asn Leu Glu Val Glu Glu Leu Lys
275 280 285

His Pro Arg Ala Gly Cys Lys Ile Lys Phe Ile Phe Gln Gly Asn Pro
240 245 300

Tyr Phe Arg Asn Glu Gly Leu Val Lys Glu Tyr Glu Arg Arg Ser Ser
305 310 315 320

Gly Arg Val Val Ser Leu Ser Thr Pro Ile Arg Trp His Arg Gly Gln
325 330 335

Asp Pro Gln Ala His Ile His Arg Asn Arg Glu Gly Asn Thr Ile Pro
340 345 350

Ser Phe Phe Asn Trp Phe Ser Asp His Ser Leu Leu Glu Phe Asp Arg
355 360 365

Ile Ala Glu Ile Ile Lys Gly Glu Leu Trp Pro Asn Pro Leu Gln Tyr
370 375 380

Tyr Leu Met Gly Glu Gly Pro Arg Arg Gly Ile Arg Gly Pro Pro Arg
385 390 395 400

Gln Pro Val Glu Ser Ala Arg Ser Phe Arg Phe Gln Ser Gly
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<10> 56

<11> 2643

<12> DNA

<13> Rattus sp.

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<21> CDS

<22> (1)..(301)

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Asn His Gly Ser Ala Leu His Ile Ala Ala Ser Asn Leu Cys Leu Gly
20 25 30

gcc gcc aaa tgt tta ctg gag cat ggt gcc aac cca ggg ctg agg aat 144
Ala Ala Lys Cys Leu Leu Glu His Gly Ala Asn Pro Ala Leu Arg Asn
35 40 45

cga aaa gga car gta cca gcc gaa gtg gtc cca gac ccc atg gac atg 192
Arg Lys Gly Gln Val Pro Ala Glu Val Val Pro Asp Pro Met Asp Met
50 55 60

tcc ctt gac aag gca gag gaa gcc ctg ctg gcc aag gaa ttg gtt aag 240
Ser Leu Asp Lys Ala Glu Ala Ala Leu Val Ala Lys Glu Leu Arg Thr
65 70 75 80

ctg cta gaa gag gct gtg cca ctg taa tgc acc ctt cct aaa gtc asa 288
Leu Leu Glu Gln Ala Val Pro Leu Ser Cys Thr Leu Pro Lys Val Thr
85 90 95

111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126
 Leu Phe Arg Tyr Asp Asp Val Phe Gly Asp Leu Met Leu Ser Ala Leu
 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141

142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157
 Gly Leu Arg Leu Gly Asp Arg Val Leu Leu Asp Gly Gln Lys Thr Gly
 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172

173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188
 Thr Leu Arg Ile Cys Gly Thr Thr Gln Phe Ala Ser Gly Gln Trp Val
 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203

204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219
 Gly Val Arg Tyr Phe Ile Cys Pro Pro Lys Gln Gly Leu Phe Ala Ser
 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234

235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250
 Val Ser Lys Val Ser Lys Ala Val Asp Ala Pro Pro Ser Ser Val Thr
 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265

266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281
 Ser Thr Pro Arg Thr Pro Arg Met Asp Phe Ser Arg Val Thr Gly Lys
 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297

298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313
 Gly Arg Arg Glu His Lys Gly Lys Lys Lys Ser Pro Ser Ser Pro Ser
 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328

329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344
 Leu Gly Ser Leu Gln Gln Arg Glu Gly Ala Lys Ala Glu Val Gly Asp
 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360

361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376
 Gln Val Leu Val Ala Gly Gln Asn Arg Asp Cys Ala Phe Leu Trp Glu
 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392

393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408
 Asp Arg Leu Cys Ser Arg Leu Leu Val Trp His
 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424

425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440
 Gln Val Leu Val Ala Gly Gln Asn Arg Asp Cys Ala Phe Leu Trp Glu
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457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472
 Asp Arg Leu Cys Ser Arg Leu Leu Val Trp His
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489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504
 Gln Val Leu Val Ala Gly Gln Asn Arg Asp Cys Ala Phe Leu Trp Glu
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521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536
 Asp Arg Leu Cys Ser Arg Leu Leu Val Trp His
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553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568
 Gln Val Leu Val Ala Gly Gln Asn Arg Asp Cys Ala Phe Leu Trp Glu
 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584

585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600
 Asp Arg Leu Cys Ser Arg Leu Leu Val Trp His
 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616

617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632
 Gln Val Leu Val Ala Gly Gln Asn Arg Asp Cys Ala Phe Leu Trp Glu
 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648

649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664
 Asp Arg Leu Cys Ser Arg Leu Leu Val Trp His
 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680

681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696
 Gln Val Leu Val Ala Gly Gln Asn Arg Asp Cys Ala Phe Leu Trp Glu
 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712

713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728
 Asp Arg Leu Cys Ser Arg Leu Leu Val Trp His
 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744

745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760
 Gln Val Leu Val Ala Gly Gln Asn Arg Asp Cys Ala Phe Leu Trp Glu
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777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792
 Asp Arg Leu Cys Ser Arg Leu Leu Val Trp His
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809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824
 Gln Val Leu Val Ala Gly Gln Asn Arg Asp Cys Ala Phe Leu Trp Glu
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841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856
 Asp Arg Leu Cys Ser Arg Leu Leu Val Trp His
 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872

873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888
 Gln Val Leu Val Ala Gly Gln Asn Arg Asp Cys Ala Phe Leu Trp Glu
 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904

905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920
 Asp Arg Leu Cys Ser Arg Leu Leu Val Trp His
 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936

937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952
 Gln Val Leu Val Ala Gly Gln Asn Arg Asp Cys Ala Phe Leu Trp Glu
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969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984
 Asp Arg Leu Cys Ser Arg Leu Leu Val Trp His
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1421
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<210> 57

<211> 267

<212> PRT

<213> Rattus sp.

<400> 57

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Asn His Gly Ser Ala Leu His Ile Ala Ala Ser Asn Leu Cys Leu Gly
 21 25 29 33 37

Ala Ala Lys Cys Leu Leu His His Gly Ala Asn Pro Ala Leu Arg Asp
 41 45 49 53

Arg Lys Gly Gln Val Pro Ala Glu Val Val Pro Asp Pro Met Asp Met
 50 55 60
 Ser Leu Asn Lys Ala Glu Ala Ala Leu Val Ala Lys Gln Leu Arg Thr
 65 70 75 80
 Leu Leu Glu Glu Ala Val Pro Leu Ser Cys Thr Leu Pro Lys Val Thr
 85 90 95
 Leu Pro Asn Tyr Asp Asn Val Pro Gly Asn Leu Met Leu Ser Ala Leu
 100 105 110
 Gly Leu Arg Leu Gly Asp Arg Val Leu Leu Asp Gly Gln Lys Thr Gly
 115 120 125
 Thr Leu Arg Phe Cys Gly Thr Thr Glu Phe Ala Ser Gly Gln Trp Val
 130 135 140
 Gly Val Glu Leu Asp Glu Pro Glu Gly Lys Asn Asp Gly Ser Val Gly
 145 150 155 160
 Gly Val Arg Tyr Phe Ile Cys Pro Pro Lys Gln Gly Leu Phe Ala Ser
 165 170 175
 Val Ser Lys Val Ser Lys Ala Val Asp Ala Pro Pro Ser Ser Val Thr
 180 185 190
 Ser Thr Pro Arg Thr Pro Arg Met Asp Phe Ser Arg Val Thr Gly Lys
 195 200 205
 Gly Arg Arg Glu His Lys Gly Lys Lys Lys Ser Pro Ser Ser Pro Ser
 210 215 220
 Leu Gly Ser Leu Gln Gln Arg Glu Gly Ala Lys Ala Glu Val Gly Asp
 225 230 235 240
 Gln Val Leu Val Ala Gly Gln Asn Arg Asp Cys Ala Phe Leu Trp Glu
 245 250 255
 Asp Arg Leu Cys Ser Arg Leu Leu Val Trp His
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<211> 2929

<212> DNA

<213> Rattus sp.

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<221> CDS

<222> (1)..(810)

<400> 58

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 Ala Asp Ser Thr Ser Arg Trp Ala Glu Ala Leu Arg Glu Ile Ser Gly
 1 5 10 15

cgc tta ttt gaa atg att gaa tat agt gga tat ttt gaa tat att ggt 96
 Arg Leu Ala Glu Met Pro Ala Asp Ser Gly Tyr Pro Ala Tyr Leu Gly
 20 25 30

| | |
|---|-----|
| acc cga ctg ggt tat ttc tat aag cga gaa aac agt ctg aac ttt | 144 |
| Ala Arg Leu Ala Ser Ile Tyr Glu Arg Ala Gly Arg Val Lys Tyr Leu | |
| 85 40 45 | |
| gga aac ctt tag aac gaa ggg att ttc agt att gta gaa gaa gtt tat | 146 |
| Gly Asn Pro Glu Arg Glu Gly Ser Val Ser Ile Val Gly Ala Val Ser | |
| 50 55 60 | |
| cca cct ggt ggt gat ttt tct gat cca gaa aca tct ggt aat ctg ggt | 240 |
| Pro Pro Gly Gly Asp Phe Ser Asp Pro Val Thr Ser Ala Thr Leu Gly | |
| 65 70 75 80 | |
| att gtt cag gtg ttc tgg ggc ttg gat aag aag cta ggt cag cga aag | 288 |
| Ile Val Gln Val Phe Trp Gly Leu Asp Lys Lys Leu Ala Gln Arg Lys | |
| 85 90 95 | |
| cac ttc ccg tcc gtc aac tgg ctc att agc tac agc aag tac atg cgc | 336 |
| His Phe Pro Ser Val Asn Trp Leu Ile Ser Tyr Ser Lys Tyr Met Arg | |
| 100 105 110 | |
| gcc ctg gac gag tac tat gac aaa cac ttc aca gag ttc gtg cct ctg | 384 |
| Ala Leu Asp Glu Tyr Tyr Asp Lys His Phe Thr Glu Phe Val Pro Leu | |
| 115 120 125 | |
| agg acc aaa gct aag gag att ctg cag gaa gag gag gat ctg gcg gaa | 432 |
| Arg Thr Lys Ala Lys Glu Ile Leu Gln Glu Glu Glu Asp Leu Ala Glu | |
| 130 135 140 | |
| atc gtg cag ctc gtg gga aag ggc tct tta gca gag aca gat aaa atc | 480 |
| Ile Val Gln Leu Val Gly Lys Ala Ser Leu Ala Glu Thr Asp Lys Ile | |
| 145 150 155 160 | |
| acc ctg gag gta gca aaa ctt atc aaa gat gac ttc cta caa caa aat | 528 |
| Thr Leu Glu Val Ala Lys Leu Ile Lys Asp Asp Phe Leu Gln Gln Asn | |
| 165 170 175 | |
| ggg tac act cct tat gac agg ttc tgt cca ttc tat aag aag gtg ggg | 576 |
| Gly Tyr Thr Pro Tyr Asp Arg Phe Cys Pro Phe Tyr Lys Thr Val Gly | |
| 180 185 190 | |
| atg ctg tcc aac atg att tca ttc tat gat atg gcc cgc cgg gct gtg | 624 |
| Met Leu Ser Asn Met Ile Ser Phe Tyr Asp Met Ala Arg Arg Ala Val | |
| 195 200 205 | |
| gag acc acc gcc cag agt gac aat aag atc aca tgg tcc att atc cgt | 672 |
| Glu Thr Thr Ala Gln Ser Asp Asn Lys Ile Thr Trp Ser Ile Ile Arg | |
| 210 215 220 | |
| gag cac atg ggg gag att ctc tat aaa ctt tcc tcc atg aaa ttc aag | 720 |
| Glu His Met Gly Glu Ile Leu Tyr Lys Leu Ser Ser Met Lys Phe Lys | |
| 225 230 235 240 | |
| gat cca gtg aag gat ggt gag gca aag atc aag ggt gat tcc cca cag | 768 |
| Asp Pro Val Lys Asp Gly Glu Ala Lys Ile Lys Ala Asp Tyr Ala Gln | |
| 245 250 255 | |
| ctt ctt gaa gat atg cag aat gaa ttc agt agt ctg gaa gat | 816 |
| Leu Leu Glu Asp Met Gln Asn Ala Phe Arg Ser Leu Glu Asp | |
| 260 265 270 | |

[illegible]

<210> 59
<211> 270
<212> FRT
<213> Rattus sp.

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          20              25              30
Ala Arg Leu Ala Ser Phe Tyr Glu Arg Ala Gly Arg Val Lys Cys Leu
          35              40              45
Gly Asn Pro Glu Arg Glu Gly Ser Val Ser Ile Val Gly Ala Val Ser
  50              55              60
Pro Pro Gly Gly Asp Phe Ser Asp Pro Val Thr Ser Ala Thr Leu Gly
  65              70              75              80
Ile Val Gln Val Phe Trp Gly Leu Asp Lys Lys Leu Ala Gln Arg Lys
          85              90              95
His Phe Pro Ser Val Asn Trp Leu Ile Ser Tyr Ser Lys Tyr Met Arg
          100             105             110
Ala Leu Asp Glu Tyr Tyr Asp Lys His Phe Thr Glu Phe Val Pro Leu
  115             120             125
Arg Thr Lys Ala Lys Glu Ile Leu Gln Glu Glu Glu Asp Leu Ala Glu
  130             135             140
Ile Val Gln Leu Val Gly Lys Ala Ser Leu Ala Glu Thr Asp Lys Ile
  145             150             155             160
Thr Leu Glu Val Ala Lys Leu Ile Lys Asp Asp Phe Leu Gln Gln Asn
          165             170             175
Gly Tyr Thr Pro Tyr Asp Arg Phe Cys Pro Phe Tyr Lys Thr Val Gly
          180             185             190
Met Leu Ser Asn Met Ile Ser Phe Tyr Asp Met Ala Arg Arg Ala Val
          195             200             205
Ile Thr Thr Ala Gln Ser Asp Asn Lys Ile Thr Trp Ser Ile Ile Arg
  210             215             220

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Val His Met Gly Glu Ile Leu Tyr Lys Leu Ser Ser Met Lys Ile Lys
225 235 235 245

Asp Pro Val Lys Asp Gly Ala Ala Lys Ile Lys Ala Asp Tyr Ala Gln
245 255 265

Leu Leu Gln Asp Met Gln Asp Ala Phe Arg Ser Leu Gln Asp
275 285 295

cd11 - 60
cd11 - 1489
cd12 - 1000
cd13 - Rattus sp.

cd20 -
cd21 - CDS
cd22 - (1)...(1058)

cd400 - 60

gaa agc cag gag gaa gag gag gat gag gaa gag gag gaa gaa cta taa 45
Ala Arg Leu Pro Ala Pro Glu His Ala Arg Gln Gln Pro Leu Leu Ser
1 5 10 15

ggc cat gag ccc gga tgg tcc gac cgg gtt cca gtt ccc ggc gtg gcc 96
Gly Pro Glu Pro Gly Ser Ser Ala Arg Val Pro Val Pro Gly Val Ala
20 25 30

agt agg cgg cag ccg gga ggc ggc aag cca ccc agc cgg gac ggc ctg 144
Ser Arg Arg Gln Pro Arg Gly Gly Lys Pro Pro Ser Gly Asp Gly Leu
35 40 45

gag tgg ggc ccc tct cca cgc cct ctt ctc cac ggc cgc ggc gag gaa 192
Glu Ser Gly Pro Ser Pro Arg Pro Leu Leu His Ala Arg Gly Glu Ala
50 55 60

ggg ctc cac cgc cag tct gga agg gtt cca cat aca gga agc gcc taa 240
Gly Leu His Arg Gln Ser Gly Arg Val Pro His Thr Gly Thr Ala Tyr
65 70 75 80

tta gaa gat gag ccc acc gag gat gag ggt ccg ggc gga tta ttt gta 288
Phe Ala Asp Gln Pro Thr Glu Ala Gln Ala Pro Gly Gly Phe Cys Val
85 90 95

tca ctc tgg ctc ctt ggg gtc cgc tgg ccg gcc tgt gac aac cgg aag 336
Ser Pro Ser Leu Leu Gly Val Arg Trp Pro Ala Cys Ala Thr Arg Thr
100 105 110

tac ggc taa ctg cat ctg tct ccc cca tca gag cag ccc cgg agc cta 384
Pro Gly Ser Leu Pro Leu Ser Pro Pro Ser Ala Gln Pro Arg Thr Leu
115 120 125

tgg ccc aac cct cca ggt ggc tca taa agt agg atg gaa gaa ctt aat 432
Trp Pro Thr Pro Pro Ala Gly Pro Ser Ser Arg Met Val Ala Arg Asn
135 140 145

tat tta gaa gaa gaa gat tat tgg att tta tta tta tta tta tta tta 480
Gln Val Ala Ala Asp Asn Ala Ile Ser Pro Ala Ser Gln Pro Arg Arg
145 150 155 160

[illegible]

Gln Ser Asp Gln Ser Thr Ser Gln Pro Ser Ser Ser Ser Ser Thr Gln
 Ala Arg Pro Arg Pro Cys Pro Val Val Pro Ala Pro Ala Pro Gly Asp
 140 180 190

act caa tta cga acc tta cga taa caa tat gat taa cga cga ata aag 624
Thr His Phe Arg Thr Phe Arg Ser His Ser Asp Tyr Arg Arg Ile Thr
195 200 205

Ggg acc agc gct ctc ctg gac gcc tgc ggc ttc tac tgg gga ccc ctg 672
 Arg Thr Ser Ala Leu Leu Asp Ala Cys Gly Phe Tyr Trp Gly Pro Leu
 210 215 220

agc gtg cat ggg ggc cac jaa cgg ctg cgt gcc gag ccc gtg ggc acc 720
 Ser Val His Gly Ala His Glu Arg Leu Arg Ala Glu Pro Val Gly Thr
 225 230 235 240

ttc ttg gtg cgc gac agt tgc cag cgg aac tgc ttc ttc ggc ttc agc 768
Phe Leu Val Arg Asp Ser Arg Gln Arg Asn Cys Phe Phe Ala Leu Ser
245 250 255

gtg aag atg gct tgg ggc ccc acg agc att cgt gtg cac ttc cag gcc 816
Val Lys Met Ala Ser Gly Pro Thr Ser Ile Arg Val His Phe Gln Ala
260 265 270

ggc cgc ttc cac ctg gac ggc agc cgc gag acc ttc gac tgc ctc ttc 864
Gly Arg Phe His Leu Asp Gly Ser Arg Glu Thr Phe Asp Cys Leu Phe
275 280 285

gag ctg ctg gag cac tac ctg gag gag cag cgc cgc atg ttg ggg ggc 912
Glu Leu Leu Glu His Tyr Val Ala Ala Pro Arg Arg Met Leu Gly Ala
290 295 300

cca ctg cgc cag cgc cgc ctg cgg cgg ctg cag gag ctg tgt cgc cag 960
 Pro Leu Arg Gln Arg Arg Val Arg Pro Leu Gln Glu Leu Cys Arg Gln
 305 310 315 320

ccc atc gtc gcc gcc gtc ggt cgc gag aac ctg gca cgc atc cct ctt 1008
Arg Ile Val Ala Ala Val Gly Arg Glu Asn Leu Ala Arg Ile Pro Leu
325 330 335

aac cgg gta ctc cgt gac tac ctg agt tcc ttc ccc ttc cag atc 1053
 Asn Pro Val Leu Arg Asp Tyr Leu Ser Ser Phe Pro Phe Gln Ile
 340 345 350

tgaccgggtg cgcgcgtgac cgcagcatta agtgggagcg ccttattatt tcttattatt 1113

aattattatt atttttttgg aaacacgggg jagatsterc egastaggtc gjaaggarrr 1173

gggtgtggagg a' gggatgoc tggacat' at ggtgggagac attatocggg gttttggggg 1233

gesteacste etjygetee eteacjyee eotaggttjt agcagettjt gietnyyee 1293

4444307 744 21 2109 11 407 27001 1574 24 15 00000000 00000000 1993

csaggyjtjt jtttjtjt sttttttt tttttttt ttatttttt ttatttttt 1413

2354

4400- 61

| | | | | |
|---|-----|-----|-----|-----|
| Ala Arg Leu Pro Ala Pro Glu His Ala Arg Gln Gln Pro Leu Leu Ser | 1 | 5 | 10 | 15 |
| Gly Pro Glu Pro Gly Ser Ser Ala Arg Val Pro Val Pro Gly Val Ala | 20 | 25 | 30 | |
| Ser Arg Arg Gln Pro Arg Gly Gly Lys Pro Pro Ser Gly Asp Gly Leu | 35 | 40 | 45 | |
| Glu Ser Gly Pro Ser Pro Arg Pro Leu Leu His Ala Arg Gly Glu Ala | 50 | 55 | 60 | |
| Gly Leu His Arg Gln Ser Gly Arg Val Pro His Thr Gly Thr Ala Tyr | 65 | 70 | 75 | 80 |
| Phe Ala Asp Glu Pro Thr Glu Ala Gln Ala Pro Gly Gly Phe Cys Val | 85 | 90 | 95 | |
| Ser Pro Ser Leu Leu Gly Val Arg Trp Pro Ala Cys Ala Thr Arg Thr | 100 | 105 | 110 | |
| Pro Gly Ser Leu Pro Leu Ser Pro Pro Ser Ala Gln Pro Arg Thr Leu | 115 | 120 | 125 | |
| Trp Pro Thr Pro Pro Ala Gly Pro Ser Ser Arg Met Val Ala Arg Asn | 130 | 135 | 140 | |
| Gln Val Ala Ala Asp Asn Ala Ile Ser Pro Ala Ser Glu Pro Arg Arg | 145 | 150 | 155 | 160 |
| Arg Pro Glu Pro Ser Ser Ser Ser Ser Ser Ser Ser Pro Ala Ala Pro | 165 | 170 | 175 | |
| Ala Arg Pro Arg Pro Cys Pro Val Val Pro Ala Pro Ala Pro Gly Asp | 180 | 185 | 190 | |
| Thr His Phe Arg Thr Phe Arg Ser His Ser Asp Tyr Arg Arg Ile Thr | 195 | 200 | 205 | |
| Arg Thr Ser Ala Leu Leu Asp Ala Cys Gly Phe Tyr Trp Gly Pro Leu | 210 | 215 | 220 | |
| Ser Val His Gly Ala His Glu Arg Leu Arg Ala Glu Pro Val Gly Thr | 225 | 230 | 235 | 240 |
| Phe Leu Val Arg Asp Ser Arg Gln Arg Asn Cys Phe Phe Ala Leu Ser | 245 | 250 | 255 | |
| Val Lys Met Ala Ser Gly Pro Thr Ser Ile Arg Val His Phe Gln Ala | 260 | 265 | 270 | |

Gly Arg Phe His Leu Asp Gly Ser Arg Glu Thr Phe Asp Cys Leu Phe
275 280 285

Glu Leu Leu Glu His Tyr Val Ala Ala Pro Arg Arg Met Leu Gly Ala
290 295 300

Pro Leu Arg Gln Arg Arg Val Arg Pro Leu Glu Glu Leu Cys Arg Gln
305 310 315 320

Arg Ile Val Ala Ala Val Gly Arg Glu Asn Leu Ala Arg Ile Pro Leu
325 330 335

Asn Pro Val Leu Arg Asp Tyr Leu Ser Ser Phe Pro Phe Gln Ile
340 345 350

<210> 62

<211> 1194

<212> DNA

<213> Rattus sp.

<220>

<221> CDS

<222> (130)..(765)

<400> 62

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ccccgggtcc cggcgccagc gcagccccgg acgatatggc ccacccctcc agctggcccc 120

tggagttagg atg gta gca cgt aac cag gtg gca gcc gac aat gcg atc tcc 171
Met Val Ala Arg Asn Gln Val Ala Ala Asp Asn Ala Ile Ser
1 5 10

cgg gca tca gag ccc cga cgg cgg cca gag cca tcc tgg tcc tgg tct 219
Pro Ala Ser Glu Pro Arg Arg Arg Pro Glu Pro Ser Ser Ser Ser Ser
15 20 25 30

tgg tcc tgg ccg gcg gcc ccg gcg cgt ccc cgg ccc tgc ccg gtg gtc 267
Ser Ser Ser Pro Ala Ala Pro Ala Arg Pro Arg Pro Cys Pro Val Val
35 40 45

cgg gcc ccg gct ccg ggc gac act cac ttc cgc acc ttc cgc tcc cac 315
Pro Ala Pro Ala Pro Gly Asp Thr His Phe Arg Thr Phe Arg Ser His
50 55 60

tct gat tac cgg cgc atc acg cgg acc agc gct ctg ctg gac gcc tgc 363
Ser Asp Tyr Arg Arg Ile Thr Arg Thr Ser Ala Leu Leu Asp Ala Cys
65 70 75

gac ttc tac tgg gga ccc ctg agc ggg cat ggg ggg car gaa cgg ctg 411
Gly Phe Tyr Trp Gly Pro Leu Ser Val His Gly Ala His Glu Arg Leu
80 85 90

cgt gcc gag ccc gtg ggc acc ttc ttg gtg cgc gac agt car cag cgg 469
Arg Ala Glu Pro Val Gly Thr Phe Leu Val Arg Asp Ser Arg Gln Arg
95 100 105 110

Aac Agt ttt ttt ttt ttt agc ttt aat atg ggt ttt ggc ttt aat agt 107
 Asn Cys Phe Ile Ala Leu Phe Val Lys Met Ala Ser Gly Iro Thr Ser
 115 120 125

att agt gta aat ttt gag gaa gaa ggt ttt aat atg gat ggt agt aat 133
 Ile Arg Val His Phe Gln Ala Gly Arg Phe His Leu Asp Gly Ser Arg
 130 135 140

gag aat ttt gag tgc ttc ttt gag atg atg gag aat ttt gta ggt ggc 603
 Glu Thr Phe Asp Cys Leu Phe Glu Leu Leu Glu His Tyr Val Ala Ala
 145 150 155

cag cgc cgc atg ttg ggt ggc cca atg cgc cag cgc cgc gta cgt cgt 651
 Pro Arg Arg Met Leu Gly Ala Pro Leu Arg Arg Arg Val Arg Pro
 160 165 170

atg cag gag atg tgt cgc cag cgc atc gta ggc ggc gta ggt cgc gag 699
 Leu Gln Glu Leu Cys Arg Gln Arg Ile Val Ala Ala Val Gly Arg Glu
 175 180 185 190

aac atg gaa cgc atc cct ctt aac cag gta ttc cgt gac ttt atg agt 747
 Asn Leu Ala Arg Ile Pro Leu Asn Pro Val Leu Arg Asp Tyr Leu Ser
 195 200 205

tcc ttc ccc ttc cag atc tgaccgggtg ccgcggtgcc cgcagcatta 795
 Ser Phe Pro Phe Gln Ile
 210

agtgggagcg ccttattatt tcttattatt aattattatt attttttctgg aaccacgtgg 855

gagccctccc cgcctaggtc ggaggagtg ggtgtggagg gtgagatgcc tccactttct 915

ggctggagac cttatccccc ctctcggggg gcctccccc ctggtgctcc ctcacgggtcc 975

ccctgggtgt agcagcttgt gctcggggcc aggacctgaa ctcacgcct acctctccat 1035

gtttacatgt tccagttatc ttgcacaaa ccagggggtgg gggagggtct ctggttccat 1095

ttttctgtg tgcagaatat tctattttat attttttacat ccagtttaga taataaaactt 1155

tattatgaaa gttttttttt taaaaaaaaa aaaaaaaaaa 1194

<210> 63

<211> 212

<212> FRT

<213> Rattus sp.

<400> 63

Met Val Ala Arg Asn Gln Val Ala Ala Asp Asn Ala Ile Ser Pro Ala
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Ser Glu Pro Arg Arg Arg Pro Glu Pro Ser Ser Ser Ser Ser Ser
 20 25 30

Ser Pro Ala Ala Pro Ala Arg Pro Arg Pro Cys Pro Val Val Pro Ala
 35 40 45

Pro Ala Pro Gly Asp Thr His Phe Arg Thr Phe Arg Ser His Ser Asp
 50 55 60

Tyr Arg Arg Ile Thr Arg Thr Ser Ala Leu Leu Asp Ala Cys Gly Ile
 65 70 75 80
 Tyr Trp Gly Pro Leu Ser Val His Gly Ala His Glu Arg Leu Arg Ala
 85 90 95
 Glu Pro Val Gly Thr Phe Leu Val Arg Asp Ser Arg Glu Arg Asn Cys
 100 105 110
 Phe Phe Ala Leu Ser Val Lys Met Ala Ser Gly Pro Thr Ser Ile Arg
 115 120 125
 Val His Phe Gln Ala Gly Arg Phe His Leu Asp Gly Ser Arg Glu Thr
 130 135 140
 Phe Asp Cys Leu Phe Glu Leu Leu Glu His Tyr Val Ala Ala Pro Arg
 145 150 155 160
 Arg Met Leu Gly Ala Pro Leu Arg Gln Arg Arg Val Arg Pro Leu Gln
 165 170 175
 Glu Leu Cys Arg Gln Arg Ile Val Ala Ala Val Gly Arg Glu Asn Leu
 180 185 190
 Ala Arg Ile Pro Leu Asn Pro Val Leu Arg Asp Tyr Leu Ser Ser Phe
 195 200 205
 Pro Phe Gln Ile
 210

<210> 64

<211> 600

<212> DNA

<213> Rattus sp.

<220>

<221> CDS

<222> (52)..(336)

<400> 64

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 tac caa atg gag cat gcc atg gaa acc atg atg att asa ttt car agg 105
 Ser Gln Met Glu His Ala Met Glu Thr Met Met Leu Thr Phe His Arg
 5 10 15
 ttt gaa ggg gaa aaa aac tac ttg asa aag gag gac ctg aga atg ctg 183
 Phe Ala Gly Glu Lys Asn Tyr Leu Thr Lys Glu Asp Leu Arg Val Leu
 20 25 30
 atg gaa agg gag ttg cat ggg ttt ttg gaa aat caa aag cac att ctg 261
 Met Glu Arg Glu Phe Pro Gly Phe Leu Glu Asn Gln Lys Asp Pro Leu
 35 40 45 50

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344 gta gaa gaa gaa gaa gaa gaa gaa gaa gaa gaa gaa gaa gaa gaa gaa 348
Ala Val Asp Lys Ile Met Lys Asp Leu Asp Gln Cys Arg Asp Gly Lys
      55              60              65

349 gta gaa gaa gaa gaa gaa gaa gaa gaa gaa gaa gaa gaa gaa gaa gaa 353
Val Gly Phe Gln Ser Phe Leu Ser Leu Val Ala Gly Leu Ile Ile Ala
      70              75              80

354 tgc aat gac tat ttt gta gta cac atg aag gag aag aag taggaaact 358
Cys Asn Asp Tyr Phe Val Val His Met Lys Lys Lys
      85              90              95

ggagcaatgg taccacacac ttgatgggtc ctctcccatg gggccaactg aggaatctgc 406
cccaatgctt cctgtgagca gatcaggacc cttaggaaat gtgcaataa catccaactc 466
caatcgaca agcagagaaa gaaaagttaa tccaatgaca gaggagcttt cgagttttat 526
attggttgca tccggttgcc ctcaataaag aaagtctttt tttttaagtt ccgaaaaaaa 586
aaaaaaaaaa aaaa 600

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<210> 65
 <211> 95
 <212> PRT
 <213> Rattus sp.

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<400> 65
Met Pro Ser Gln Met Glu His Ala Met Glu Thr Met Met Leu Thr Phe
  1              5              10              15

His Arg Phe Ala Gly Glu Lys Asn Tyr Leu Thr Lys Glu Asp Leu Arg
      20              25              30

Val Leu Met Glu Arg Glu Phe Pro Gly Phe Leu Glu Asn Gln Lys Asp
      35              40              45

Pro Leu Ala Val Asp Lys Ile Met Lys Asp Leu Asp Gln Cys Arg Asp
      50              55              60

Gly Lys Val Gly Phe Gln Ser Phe Leu Ser Leu Val Ala Gly Leu Ile
      65              70              75              80

Ile Ala Cys Asn Asp Tyr Phe Val Val His Met Lys Lys Lys
      85              90              95

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<210> 66
 <211> 639
 <212> DNA
 <213> Rattus sp.

<220>
 <221> CDS
 <222> (1)..(636)

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<400> 66
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Met Ala Tyr Ala Tyr Leu Phe Lys Tyr Ile Ile Ile Gly Asp Thr Gly

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| 1 | 5 | 10 | 15 | |
|---|-----|-----|-----|-----|
| ggt ggt aat tat tgg tta ttg cta cgt ttt ata gac aat ggt ttt cag | | | | 20 |
| Val Gly Lys Ser Cys Leu Leu Leu Gln Phe Thr Asn Lys Asn Phe Gln | | | | |
| 35 | 40 | 45 | | |
| cag ggg cat gac ctc aca att ggt gta gag ttt ggt ggt ggt atg ata | | | | 144 |
| Pro Val His Asp Leu Thr Ile Gly Val Glu Phe Gly Ala Arg Met Ile | | | | |
| 35 | 40 | 45 | | |
| acc att gat ggt aaa cag ata aaa ctc cag atc tgg gat aca gca ggg | | | | 192 |
| Thr Ile Asp Gly Lys Gln Ile Lys Leu Gln Ile Trp Asp Thr Ala Gly | | | | |
| 50 | 55 | 60 | | |
| cag gag tcc ttt cgt tct atc aca agg tca tat tac aga ggt gca gcg | | | | 240 |
| Gln Glu Ser Phe Arg Ser Ile Thr Arg Ser Tyr Tyr Arg Gly Ala Ala | | | | |
| 65 | 70 | 75 | 80 | |
| ggg gct tta cta gtg tat gat att aca agg aga gac acg ttc aac cac | | | | 288 |
| Gly Ala Leu Leu Val Tyr Asp Ile Thr Arg Arg Asp Thr Phe Asn His | | | | |
| 85 | 90 | 95 | | |
| ttg aca acc tgg tta gaa gac gcc cgt cag cat tcc aat tcc aac atg | | | | 336 |
| Leu Thr Thr Trp Leu Glu Asp Ala Arg Gln His Ser Asn Ser Asn Met | | | | |
| 100 | 105 | 110 | | |
| gtc atc atg ctt att gga aat aaa agt gac tta gaa tct agg aga gaa | | | | 384 |
| Val Ile Met Leu Ile Gly Asn Lys Ser Asp Leu Glu Ser Arg Arg Glu | | | | |
| 115 | 120 | 125 | | |
| gtg aaa aag gaa gaa ggt gaa gct ttt gca cga gag cat gga ctt atc | | | | 432 |
| Val Lys Lys Glu Glu Gly Glu Ala Phe Ala Arg Glu His Gly Leu Ile | | | | |
| 130 | 135 | 140 | | |
| ttc atg gaa act tct gcc aag act gct tct aat gta gag gag gca ttt | | | | 480 |
| Phe Met Glu Thr Ser Ala Lys Thr Ala Ser Asn Val Glu Glu Ala Phe | | | | |
| 145 | 150 | 155 | 160 | |
| att aac aca gca aaa gaa att tat gaa aaa atc caa gaa ggg gtc ttt | | | | 528 |
| Ile Asn Thr Ala Lys Glu Ile Tyr Gln Lys Ile Gln Glu Gly Val Phe | | | | |
| 165 | 170 | 175 | | |
| gac att aat aat gag gca aac ggc atc aaa att ggc cct cag cat gct | | | | 576 |
| Asp Ile Asn Asn Glu Ala Asn Gly Ile Lys Ile Gly Pro Gln His Ala | | | | |
| 180 | 185 | 190 | | |
| gct acc aat gca tct cac gga ggc aac caa gga ggg cag cag gaa ggg | | | | 624 |
| Ala Thr Asn Ala Ser His Gly Gly Asn Gln Gly Gly Gln Gln Ala Gly | | | | |
| 195 | 200 | 205 | | |
| gta tta tga tta tga | | | | 639 |
| Gly Gly Cys Cys | | | | |
| 210 | | | | |

<210> 6"

<211> 212

<212> FRT

<213> Rattus sp.

<400> 67

Met Ala Tyr Ala Tyr Leu Phe Lys Tyr Ile Ile Ile Gly Asp Thr Gly
1 5 10 15Val Gly Lys Ser Cys Leu Leu Leu Gln Phe Thr Asp Lys Arg Phe Gln
20 25 30Pro Val His Asp Leu Thr Ile Gly Val Glu Phe Gly Ala Arg Met Ile
35 40 45Thr Ile Asp Gly Lys Gln Ile Lys Leu Gln Ile Trp Asp Thr Ala Gly
50 55 60Gln Glu Ser Phe Arg Ser Ile Thr Arg Ser Tyr Tyr Arg Gly Ala Ala
65 70 75 80Gly Ala Leu Leu Val Tyr Asp Ile Thr Arg Arg Asp Thr Phe Asn His
85 90 95Leu Thr Thr Trp Leu Glu Asp Ala Arg Gln His Ser Asn Ser Asn Met
100 105 110Val Ile Met Leu Ile Gly Asn Lys Ser Asp Leu Glu Ser Arg Arg Glu
115 120 125Val Lys Lys Glu Glu Gly Glu Ala Phe Ala Arg Glu His Gly Leu Ile
130 135 140Phe Met Glu Thr Ser Ala Lys Thr Ala Ser Asn Val Glu Glu Ala Phe
145 150 155 160Ile Asn Thr Ala Lys Glu Ile Tyr Glu Lys Ile Gln Glu Gly Val Phe
165 170 175Asp Ile Asn Asn Glu Ala Asn Gly Ile Lys Ile Gly Pro Gln His Ala
180 185 190Ala Thr Asn Ala Ser His Gly Gly Asn Gln Gly Gly Gln Gln Ala Gly
195 200 205Gly Gly Cys Cys
210

<210> 68

<211> 816

<212> DNA

<213> Rattus sp.

<220>

<221> CDS

<222> (1)...(-13)

<400> 68

atg atg atg atg aag aag tat cgg atc atc atg atc atg tat gta tat 48
Met Val Leu Leu Lys Glu Tyr Arg Val Ile Leu Pro Val Ser Val Asp
1 5 10 15

| | |
|---|-----|
| atg tat taa tta tga tag tta tat ttt gta att taa taa att aat aat aat | 76 |
| Ala Tyr Ala Val Gly Ala Leu Tyr Ser Val Ala Glu Ala Ser Lys Asn | |
| 35 40 45 | |
| tta att att att ttt taa att tta att gta tag att att att att att att | 144 |
| Ala Thr Gly Gly Gly Ala Gly Val Ala Val Leu Val Asn Ala Ser Tyr | |
| 45 50 55 60 | |
| tat aat att att ttt tta aat ttt tta att tta tta att att att att att | 192 |
| Glu Lys Asp Asp Gly Ala Lys Gly Ala Tyr Thr His Lys Ile Tyr His | |
| 55 60 65 70 75 80 | |
| tta taa att aat gtt tta aat ttt tta tta att tta tta att att att att | 240 |
| Leu Glu Ser Lys Val Pro Thr Ile Val Arg Met Leu Ala Pro Glu Gly | |
| 65 70 75 80 | |
| tta tta att tta tta tta tta att tta att tta tta att att att att att | 288 |
| Ala Leu Asn Ile His Glu Lys Ala Trp Asn Ala Tyr Pro Tyr Cys Arg | |
| 85 90 95 | |
| acc gtt att aat aat gag tac atg aag gaa gac ttt ctc att aaa att | 336 |
| Thr Val Ile Thr Asn Glu Tyr Met Lys Glu Asp Phe Leu Ile Lys Ile | |
| 100 105 110 | |
| gaa acc tgg taa aag taa gac att gta acc cag gag aat gtg cat aaa | 384 |
| Glu Thr Trp His Lys Pro Asp Leu Gly Thr Gln Glu Asn Val His Lys | |
| 115 120 125 | |
| ctg gag cct gag gaa tgg aat cat gta gaa gat ata tat ata gac atc | 432 |
| Leu Glu Pro Glu Ala Trp Lys His Val Glu Ala Ile Tyr Ile Asp Ile | |
| 130 135 140 | |
| tta gat tga aat taa gta att tta att att att att att att att att | 480 |
| Ala Asp Arg Ser Gln Val Leu Ser Lys Asp Tyr Lys Ala Glu Glu Asp | |
| 145 150 155 160 | |
| caa gaa gaa ttt aaa ttt att aaa aat gga tga gga taa tta gta taa | 528 |
| Pro Ala Lys Phe Lys Ser Ile Lys Thr Gly Arg Gly Pro Leu Gly Pro | |
| 165 170 175 | |
| att tta aat tta gaa att gta att tta aat gaa gaa taa tta att att | 576 |
| Asn Trp Lys Gln Glu Leu Val Asn Gln Lys Asp Cys Pro Tyr Met Cys | |
| 180 185 190 | |
| gaa tac aat att gtt att gta aag tta aag tgg tgg ggc tta cag aac | 624 |
| Ala Tyr Lys Leu Val Thr Val Lys Phe Lys Trp Trp Gly Leu Gln Asn | |
| 195 200 205 | |
| aaa gta gaa aat att ata cat aag taa gaa aag att att att att att | 672 |
| Lys Val Gln Asn Ile Ile His Lys Gln Glu Lys Arg Leu Ile Thr Asn | |
| 210 215 220 | |
| tta att att att att att att att att att att att att att att att | 720 |
| Ile His Arg Ala Leu Ile Cys Trp Leu Asp Lys Trp Val Asp Leu Thr | |
| 225 230 235 240 | |
| att att att att att att att att att att att att att att att att | 768 |
| Met Asp Asp Ile Arg Arg Met Glu Ala Glu Thr Lys Arg Ala Leu Asp | |
| 245 250 255 | |

Gag Arg Asp Gln Ser His Lys Phe Met Thr Val Leu Ile Tyr Asn Glu
Glu Met Arg Gly Lys Asp Pro Val Lys Gly Met Thr Ala Asp Asp

260 270

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<210> 69
<211> 2263
<212> DNA
<213> Simian sp.
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 aagaaagcaa ggcagaggag cactctctcag tggctgtggt cggaccatga cctagctgac 120
 catgaacttg gaagggtctg aaatgatagc agttctgacg gtcattgtgc tttttgttaa 180
 attatttgaa cagtttggtc tgattgaagc aggtttagaa gacagcgtgg aagatgaact 240
 ggagatggcc actgtcaggc atcggcctga ggccttgag ctcttggaag cccagagcaa 300
 atttaccaaag aaagagcttc agatccttta ccagaggattt aagaacgaat gcccagtg 360
 tgttgtaaat gaagaaacct tcaaagagat ttaactgcag ttctttccac agggagactc 420
 tacaacatat gcacattttc tgttcaatgc gtttgatacg gaccacaatg gagctgtgag 480
 ttctgaggat ttcatcaaag gtctttccat ttgtctcgg gggacagtac aagaaaaact 540
 caattgggca tttaatctgt atgatataaa taaagatggc tacatcacta aagaggaaat 600
 gcttgatata atgaaagcaa tatacgacat gatgggtaaa tgtacatata ctgtctcaa 660
 agaagatgca ccagagacaac acgtcgaaac attttttcag aaaatggaca aaaataaaga 720
 tggggttgtt accatagatg agttcattga aagctgccaa aaagatgaaa acataatgcg 780
 ctccatgcag ctctttgaaa atgtgattta acttgtcaac tagatcctga atccaacaga 840
 caaatgtgaa ctattctacc acccttaaag tcggagctac cacttttagc atagattgct 900
 cagtttgaca ctgaagcata ttatgcaaac aagatttgtt ttaatatata gcaatccca 960
 aaagatttga gttctcagt tataaatttg cctcctttcc ataatgcac tgagttcatg 1020
 ggatgttcta actcatttca tactctgtga atattcaaaa gtaatagaat ctggcatata 1080
 gtcttattga ttccttagcc atgggattat tgaggcttcc acatctcagt gattttaaaa 1140
 taacagtgtt ttctgtact ccttggatg tattcagtaa taggattctg aatggttttc 1200
 taatatactg acatctgaat ttaatttcca gaattaaaat taattttcat gctggaatg 1260
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 ttaacattt aaattttt cctcagatc cagcatatg ctatctatg ctatgaaa 1440
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ttatgattt ttaatttta caggttggt ttattglat ttttaagtg agtttgaag 1160
 agttatata caaaacaaa attttttata atttttta attttttt ttatttttt 1200
 caagtatag ttaattgotta ataaatagta atattatag cattaaagg caaatctgtc 1600
 ctatttttaa tgaatttcct acagcatggt tatattttaa ggcattcagg gacaaagaaa 1740
 cettgactac cccactgtct actaggaaca aacaaacaga aagcaaaatt cactttgaaa 1800
 gaacagaggg ttccattaca ttgacaacta ctaccaagat tcagttagaa ataatgtctc 1860
 aaaaactaat ccagattaca atatgatita gtgcataata aaatttcaac aatttcagatt 1920
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<210> 70

<211> 229

<212> PRT

<213> Simian sp.

<400> 70

Met Asn Leu Glu Gly Leu Glu Met Ile Ala Val Leu Ile Val ile Val
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Leu Phe Val Lys Leu Leu Glu Gln Phe Gly Leu Ile Glu Ala Gly Leu
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Glu Asp Ser Val Glu Asp Glu Leu Glu Met Ala Thr Val Arg His Arg
 35 40 45

Pro Glu Ala Leu Glu Leu Leu Glu Ala Gln Ser Lys Phe Thr Lys Lys
 50 55 60

Glu Leu Gln Ile Leu Tyr Arg Gly Phe Lys Asn Glu Cys Pro Ser Gly
 65 70 75 80

Val Val Asn Glu Glu Thr Phe Lys Glu Ile Tyr Ser Gln Phe Phe Pro
 85 90 95

Gln Gly Asp Ser Thr Thr Tyr Ala His Phe Leu Phe Asn Ala Phe Asp
 100 105 110

Thr Asp His Asn Gly Ala Val Ser Phe Glu Asp Phe Ile Lys Gly Leu
 115 120 125

Ser Ile Leu Leu Arg Gly Thr Val Gln Glu Lys Leu Asn Trp Ala Phe
 130 135 140

Asn Leu Tyr Asp Ile Asn Lys Asp Gly Tyr Ile Thr Lys Glu Glu Met
145 150 155 16

Leu Asp Ile Met Lys Ala Ile Tyr Asp Met Met Gly Lys Cys Thr Tyr
160 170 175

Pro Val Leu Lys Glu Asp Ala Pro Arg Gln His Val Glu Thr Phe Phe
180 185 190

Gln Lys Met Asp Lys Asn Lys Asp Gly Val Val Thr Ile Asp Glu Phe
195 200 205

Ile Glu Ser Cys Gln Lys Asp Glu Asn Ile Met Arg Ser Met Gln Leu
210 215 220

Phe Glu Asn Val Ile
225

<210> 71

<211> 2259

<212> DNA

<213> Simian sp.

<400> 71

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ggcggtttcc tgtatgctca gaacagcacc aagcgcagca ttaaagagcg gctcatgaag 180
ctcttgccct gctcagctgc caaaacatcg tctctgcta ttcaaaacag cgtggaagat 240
gaactggaga tggccactgt caggcatcgg cctgaggccc ttgagcttct ggaagcccag 300
agcaaattta ccaagaaaga gcttcagatc cttacagag gatttaagaa cgaatgcccc 360
agtgggtgtg ttaatgaaga aacottcaaa gagatttact cgcagttctt tccacaggga 420
gactctacaa catatgcaca tttctgttc aatgcgtttg atcggacca caatggagct 480
gtgaqtttcg aqaatttcac caaagttctt tccattttgc tccgggggac agtanaagaa 540
aaactcaatt gggcatttaa tctgtatgat ataaataaag atggctacat cactaaagag 600
gaaatgcttg atataatgaa agcaatatac gacatgatgg gtaaatgtac atctctgtc 660
ctcaagaag atgcaccag acaacacgtc gaaacatttt ttacagaaat ggacaaaaat 720
aaagatgggg ttgttaccat agatgagttc attgaaagct gccaaaaaga tgaacacata 780
atgggtctca tgcagctctt tgaacatgtg atttaacttg tcaactagat cctgaatcca 840
acagacaaat ctgaactatt ctacacat taaagtccga gttacacatt ttgatataga 900
ttgtcagct tgaactgaa gcatattatg caaacaaagt ttgttttaat ataaagcaat 960
cccaaaaaga tttagtttc taattatca atttgcatc attttatc tcaattgagt 1020
tcattgggat ttctgaatca ttctacatc ttgtgaatatt caaaagtaac agaattctgg 1080

[illegible]

- *210 = 70
- *211 = 250
- *212 = FRT
- *213 = Similar: SE

04098-72

Met Asn Val Arg Arg Val Glu Ser Ile Ser Ala Glu Leu Glu Glu Ala
1 4 10 15

Ser Ser Thr Gly Gly Phe Leu Tyr Ala Glu Asn Ser Thr Lys Arg Ser
2 7 13

Ile Lys Glu Arg Leu Met Lys Leu Leu Pro Cys Ser Ala Ala Lys Thr
31 40 46

Ser Ser Pro Ala Ile Glu Asn Ser Val Glu Asp Glu Leu Glu Met Ala
51 57 63

Thr Val Arg His Arg Pro Glu Ala Leu Ala Leu Leu His Ala His Ser
69 74 85 91

Lys His Thr Lys Lys His Leu His Ile Leu Tyr Arg Gly Phe Lys Asn
 85 95
 His Cys Pro Ser Gly Val Val Asn Gly Glu Thr Phe Lys Glu Ile Tyr
 1 105
 Ser His Phe Phe Pro His Gly Asp Ser Thr Thr Tyr Ala His Phe Leu
 115 125
 Phe Asn Ala Phe Asp Thr Asp His Asn Gly Ala Val Ser Phe Glu Asp
 135 145
 Phe Ile Lys Gly Leu Ser Ile Leu Leu Arg Gly Thr Val Glu Glu Lys
 155 165
 Leu Asn Trp Ala Phe Asn Leu Tyr Asp Ile Asn Lys Asp Gly Tyr Ile
 165 175
 Thr Lys Glu Glu Met Leu Asp Ile Met Lys Ala Ile Tyr Asp Met Met
 185 195
 Gly Lys Cys Thr Tyr Pro Val Leu Lys Glu Asp Ala Pro Arg Glu His
 195 205
 Val Glu Thr Phe Phe Glu Lys Met Asp Lys Asn Lys Asp Gly Val Val
 215 225
 Thr Ile Asp Glu Phe Ile Glu Ser Cys Glu Lys Asp Glu Asn Ile Met
 235 245
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